

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2003, 02:31:15 / Search time 142 Seconds
(without alignments)
2475.011 Million cell updates/sec

Title: US-08-908-453-1

Perfect score: 6046

Sequence: 1 MHVILHPOLQTMVEQWQMR.....AFNGSWSTKWLFLHAVRHY 1146

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 segs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-NO_XLIPY -NO_MMAP -LARGEXURY -NEG_SCORES=0 -WAIT_DSPELLOCK=100 -LONGLOC
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-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6046	100.0	3504	4	US-08-857-076-47 Sequence 47, Appl
2	1089	18.0	3207	1	US-08-162-081B-35 Sequence 35, Appl
3	1089	18.0	3207	2	US-08-780-872-35 Sequence 35, Appl
4	1089	18.0	3207	4	US-09-085-957-35 Sequence 35, Appl
5	1082	17.9	3240	1	US-08-162-081B-34 Sequence 34, Appl
6	1082	17.9	3240	4	US-08-780-872-34 Sequence 34, Appl
7	1082	17.9	3240	4	US-09-085-957-34 Sequence 34, Appl
8	1079	17.8	3412	1	US-08-162-081B-32 Sequence 32, Appl
9	1079	17.8	3412	2	US-08-780-872-32 Sequence 32, Appl
10	1079	17.8	3412	4	US-09-085-957-32 Sequence 32, Appl
11	1038	17.2	3808	2	US-08-916-917-3 Sequence 3, Appl
12	1038	17.2	3808	2	US-08-972-631-3 Sequence 3, Appl

13	1038	17.2	3808	2	US-08-972-629-3	Sequence 3, Appl
14	1038	17.2	3808	2	US-08-972-630-3	Sequence 3, Appl
15	1038	17.2	3808	2	US-08-672-211-3	Sequence 3, Appl
16	1038	17.2	3808	3	US-09-225-170-3	Sequence 3, Appl
17	1035	17.1	3213	3	US-09-392-350-1	Sequence 1, Appl
18	1033	17.1	5220	2	US-08-777-405A-1	Sequence 1, Appl
19	1033	17.1	5220	2	US-08-977-871A-1	Sequence 1, Appl
20	1033	17.1	5220	2	US-09-225-951-1	Sequence 1, Appl
21	1031	17.1	3868	3	US-09-357-070-1	Sequence 1, Appl
22	1015	16.8	5162	2	US-08-916-917-13	Sequence 13, Appl
23	1015	16.8	5162	3	US-09-225-170-13	Sequence 13, Appl
24	1002	16.6	4134	2	US-08-817-090B-3	Sequence 3, Appl
25	1002	16.6	4134	2	US-08-817-090B-1	Sequence 1, Appl
26	639	10.6	5285	2	US-08-609-049A-29	Sequence 29, Appl
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28	624	10.3	5061	4	US-09-355-160D-1	Sequence 1, Appl
29	622.5	10.3	6831	2	US-08-609-049A-27	Sequence 27, Appl
30	622.5	10.3	6831	4	US-09-170-996-27	Sequence 27, Appl
31	551.5	9.1	3252	4	US-09-118-442-1	Sequence 1, Appl
32	551.5	9.1	3252	4	US-09-677-064-1	Sequence 1, Appl
33	257.5	4.3	393	1	US-08-162-081B-40	Sequence 40, Appl
34	257.5	4.3	393	2	US-08-780-872-40	Sequence 40, Appl
35	257.5	4.3	393	4	US-09-085-957-40	Sequence 40, Appl
36	257.5	4.3	2451	2	US-08-820-170A-29	Sequence 29, Appl
37	257.5	4.3	2451	3	US-09-055-659-29	Sequence 29, Appl
38	257.5	4.3	2451	4	US-09-273-555-29	Sequence 29, Appl
39	257.5	4.3	2451	4	US-09-565-538-29	Sequence 29, Appl
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41	257.5	4.3	2487	2	US-08-820-170A-32	Sequence 32, Appl
42	257.5	4.3	2487	3	US-09-055-659-32	Sequence 32, Appl
43	257.5	4.3	2487	4	US-09-273-555-32	Sequence 32, Appl
44	257.5	4.3	2487	4	US-09-565-538-32	Sequence 32, Appl
45	257.5	4.3	2487	4	US-09-661-468-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-857-076-47
Sequence 47, Application US/08857076C
Patent No. 6225120
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
APPLICANT: Ogg, Scott
APPLICANT: Paradis, Suzanne
APPLICANT: Tissenbaum, Heidi
APPLICANT: Morris, Jason
APPLICANT: Kowsek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-08-857-076-47
ALIGNMENT Scores:
Pred. No.: 0
Score: 6046.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
US-08-908-453-1 (1-1146) x US-08-857-076-47 (1-3504)

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 QY 21 GIUARGProSerLeuG1nThrG1uAsnG1YLSG1SerLeuLeuG1uAsnG1uG1 40
 DB 124 GAACGCCCATCCGTCGAGACCGGAAATGGCAAGATCCGCTGCGAATAATGAAGT 183
 QY 41 Val1AlaSerP1Le1ThMetCysProPheG1uVal11LeSerVal1ValPheProTP 60
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 DB 544 CTGGAGAAGAGCCTCATGATGAGAACTCCCTCAATTCGTGCTTCTCGGGCTCCATG 603
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Db 2704 ATTGATTCCTGTTTGAACCCGTAAGCAAGTCTTCCAAAGGGAATATGATGATTTAT 2763
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Db 2764 GAAAGTGGCCATATTGTAACCAATATTCGAGATTCAAGTTGGAACAGAGATTCATGAT 2823
Qy ThrAlaValArgSerIleAspProSerPheMetAsnIleTyrIleArgIleGlnGly 940
Db 2824 ACGACATTCGAGATGATGATCTTCGTTAAGAAATGAGTATTCGGAACAAAGCGCA 2883
Qy IleGluAspGluValLeuIleSerIleIleAspSerThrIleAsnProIleGluIleIle 960
Db 2884 ATTGAAGTGAAGAAAGAAAGAAAGCAAGAGCTTACGAAATATCCATCAAGAAAGAG 2943
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Qy MetThrValIleArgSerGlyIleSerValAspGlyAsnSerHisGluLeuGlnIlePhe 1060
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Qy LeuPheThrLeuMetLeuGlyIleGluIleuProGluLeuSerThrIleValIleAspLeuAsp 1100
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Qy 1121 AlaGlyIleTyrGluGluAlaPheAsnGlySerIlePheThrIleAsnTyrLeuPhe 1140
Db 3424 GCTGAAATCTAGAAAGAGCCCTTCAATGATGATGATGCTTACCAAAAGCATTTGCTTTC 3483
Qy 1141 HisAlaValIleValThrIle 1146
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RESULT 2
US-08-162-081B-35
; Sequence 35, Application US/08162081B
; Patent No. 5624492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Balas, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano, Gout, Ivan Iarsovitich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08162,081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-162-081B-35

Alignment Scores:
Pred. No.: 1,01e-119 Length: 3207
Score: 1089.00 Matches: 311
Percent Similarity: 46.37% Conservative: 219
Best Local Similarity: 27.21% Mismatches: 431
Query Match: 18.01% Indels: 182
DB: Gaps: 39

US-08-908-453-1 (1-1146) x US-08-162-081B-35 (1-3207)
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Db 115 GAGGCTACGTTAATTAACATTAAGCATGAATGATTAATA-----GAAGCAAGAAATATC 168

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Db 229 GCAGAAAGGAAAGAAATTTTGTATGATAACAAGACGCTTGTGACCTTGGCTTTTTCAA 288
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Db 289 -----CCCTTTTAAAGTAATTTGAACCAAGTAGGCAACCCGTAAGAAAAGATCCCAAT 342
QY 148 SerAspIleSerHisCysLeuGlyTyrSerIleAspIleLeuGluLeuSerLeuAspGlu 167
Db 343 CCAAGAAATGGTTTCTTATCGGCATGCCAGTGTGTGAATTCGATATGCTTAAAGATCCA 402
QY 168 GluLeuArgGlnPheArgIleSerLeuTyrAlaArgThrIleLeuSerCysLeuThrArg 187
Db 403 GAAGTACAGAGACTTCCGAAAGAAATATTCATGTTGTAAAGAACTGTGATCTTAAAG 462
QY 188 GlyLeu-----GluGlyThrSerHisTyrAlaPheProGluGluGlnTyrLeuCys 204
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QY 205 ValGlyGluSerCysProIysAspLeuGluSerIleValIleAlaIleAlaIleLeuSerTyr 224
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QY 225 GlnMetPheTyr-----ArgIysArgIysAlaGluIle 235
Db 574 GTGGGATTTGGGTATAGTCTTCCAAATATGACAAACAGAAAGATATCTCGAAATC 633
QY 236 AsnGlyValCys-----GluIysMetMetIysIleGlnIleGluPheAsnProAsnGlu 253
Db 634 AACCATGACTGTGTGCCAAGACAGTAATTAATGCTGAACCATCAG-----AAAAA 684
QY 254 ThrProIysSerLeuHisTyrPheLeuTyrGluMetArgIysLeuAspValTyrAsp 273
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QY 274 ThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuAlaGlyArgThrThrPheVal 293
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QY 294 ThrAsnProAspValIysLeuThrSerTyrAspGlyValArgSerGluLeuGluSerTyr 313
Db 784 CTAGAA--AAATATCTCTGAGTCACTATTAAGTATATAAGACGTGTATATGCTTGGG 840
QY 314 ArgCysProGlyPheValValArgArgGlnSerLeuValLeuIysAspTyrCysArgPro 333
Db 841 AGGATGCCCAATTTGATGCTGATGCTTAA----- 870
QY 334 LysProLeuTyrGluProHisTyrValArgAlaHisGluArgIysLeuAlaLeuAspVal 353
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QY 354 LeuSerValSerIleAspSerThrProIysGlnSerIleAsnSerAspMetValMetThr 373
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QY 374 AspPheArgProThrAlaSerLeuLysGlnValSerLeuTyrAspLeuAspAlaAsnLeu 393
Db 949 TATATGAATGAGAAACATCTACAAA-----TCCCTTTGGGTTTAAATATGATGCAC 1002
QY 394 MetIleArg-----ProValAsnIleSerGlyPheAspPhePro 406
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QY 407 AlaAspValAspMetTyrValArgIleGluPheSerValTyrValGlyThrLeuThrLeu 426
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QY 427 AlaSerIys--SerThrThrIysValAlaAsnAlaGlnPheAlaIysTyrAsnIysGluMet 445

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QY 446 TyrThrPheAspLeuTyrMetIleAspMetProProSerAla-----ValLeuSerIle 463
Db 1159 CTGAATTCAGATATATATCATCTTCGATCTCTCTGCTGCTGCAGCTTGTGCTTTCCATT 1218
QY 464 ArgValLeuTyrGlyIysValIleLeuIysSerGluGluPheGluValGlyTyrValAsn 483
Db 1219 TGTCTGTAAAGCGGAAGGGTGTCTAAAGAGAACCTGTCCATTTGGCTGGGGAAT 1278
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QY 504 AlaProGluProThrAlaAsnArgSerArgIleGlyIleAsnGlyAlaArgIleGlyThr 523
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Db 1393 AATCCAAATTAAGAAACTCCATGTTTAAAGTTGAGTTGACTGTGATGCAGACTGTGGTA 1452
QY 539 ArgMetProSerGlnGlyGlnTyrThrTyrLeuValIysHisArgSerThrTyrThrGlu 558
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 Qy 1104 LysThrLeuPheCysAsnGlyIleuSerIlyGlnGlnAlaArgIlyPhePheAlaGlyIle 1123
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 Qy 1144 LysHisIly 1146
 Db 3187 AAGCAGCAT 3195
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 RESULT 3
 US-08-780-872-35
 ; Sequence 35, Application US/08780872
 ; Patent No. 5846824
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Balai, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Odeu, Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano, Gout, Ivan Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felte & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/780, 872
 ; FILING DATE: 09-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/162, 081
 ; FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: PCT/GB93/00761
 ; FILING DATE: 13 April 1993
 ; ATTORNEY/AGENT INFORMATION:
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 ; REGISTRATION NUMBER: 34,894
 ; REFERENCE/DOCKET NUMBER: LUD 5256
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEO ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3207 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-780-872-35
 Alignment Scores:
 Pred. No.: 1,01e-119 Length: 3207
 Score: 1089.00 Matches: 311
 Percent Similarity: 46.37% Conservative: 219
 Best Local Similarity: 27.21% Mismatches: 431
 Query Match: 18.01% Indels: 182
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 Qy 108 GYGLVLLGLVALLPHEASNSPARGINPROLEUSERLYSLEUGLULHISGLY 127
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 Qy 188 GlyLeu-----GluGlyThrSerHisTyrglnAlaPheProGluGluGlnTyrglnCys 204
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 Qy 225 GlnMetPheTrp-----ArgLysArgLysAlaGluLe 235
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 Qy 504 AlaProGluProThrAlaAsnArgSerArgIleGlyGluAsnGlyValArgIleGlyThr 523
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 Qy 524 Asn-----AlaAlaValThrIleGluIleSerSerTyrglnTyrgVal 538
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DB 3187 AAGCAGCAT 3195

RESULT 4
US-09-085-957-35
; Sequence 35, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Gout, Ivan; Masayuki, Panayotou, George; Volinia,
; APPLICANT: Stefano, Gout, Ivan; Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
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; REFERENCE/DOCKET NUMBER: LUD 5256
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; TELEFAX: (212) 838-3884
; INFORMATION FOR SEO ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-085-957-35

Alignment Scores:
Pred. No.: 1,01e-119 Length: 3207
Score: 1089.00 Matches: 311
Percent Similarity: 46.37% Conservative: 219
Best Local Similarity: 27.21% Mismatches: 431
Query Match: 18.01% Indels: 182
DB: 4 Gaps: 39

US-08-908-453-1 (1-1146) x US-09-085-957-35 (1-3207)
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DB 115 GAGGCTACGTTATATACATTAAGCATTAAGCATTAATTTATA-----GAAACAAAGAAATAC 168
QY 90 GlyThrIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 107

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Db CCTCCATCACTTCTCAAGATGAATCTTCTACATTTTGGTAACTTACCCAGAA 228
Qy 108 GylgluilegluValilepheasnsparglnProleuserLysleuGluleuHsgly 127
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Qy 128 ThrPheProMetLeuPheLeuTyrglnProasprgylleasnArgasprglnLeuMet 147
Db 289 -----CCCTTTTAAAGTAATTTGAACCACTAGGACCCGTGAAGAAAGATCTCTCAAT 342
Qy 148 SerAspIleSerHisCysleuGlyTyrgSerleuAsprgylleuGluleuSerleuAsprgln 167
Db 343 CGAAGAAATGGTTTGTCTATCGGCAGATGCGCATGTGATTCGATTTGTTAAAGTCCA 402
Qy 168 GluleuArglnPheArgAlaserleuTrpAlaArgThrLysleuThrCysleuThrArg 187
Db 403 GAAGTACAGACTCTCGAAGAAATATCTCAATGTTTGAAGACCTGTGATCTTTAG 462
Qy 188 GlyLeu-----GluGlyThrSerHisTyrgAlaPheProGluGluGlnTyrgLeuCys 204
Db 463 GATCTTAATTCACCTCATAGTAGAGCAGATGATTTTATCTTCCAAAT-----GTAGA 516
Qy 205 ValGlyGluSerCysProLysAsprglnLeuGluSerLysValLysAlaLysleuSerTyrg 224
Db 517 TCTTACCGAAGCTGCCAAGACATATATTAATTTGATTAAGCGCAATA---ATA 573
Qy 225 GlnMetPheTrp-----ArgLysArgLysAlaGluLe 235
Db 574 GTGTGATTTGGGTAAATAGTTTCTCCAAATAATGACAAACAGAAATGATCTGTGAATAAC 633
Qy 236 AsnGlyValCys-----GluLysMetMetLysIleGlnIleGluPheasnProasprgln 253
Db 634 AACCATGACTGTGTGCCAAGACAGTAATTTCTGAAGCAATCAGS-----AAAAA 684
Qy 254 ThrProLysSerleuLeuHisThrPheLeuTyrgLysMetArgLysleuAsprglnTyrgAsp 273
Db 685 ACTCGAAGTATGTGTCTATCATCT-----GAACCACTTAAACCTGTGTATTAGAA 735
Qy 274 ThrAspAspProAlaAsprglnGlyTyrgPheLeuGlnLeuAlaGlyArgThrThrPheVal 293
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Qy 294 ThrAsnProAspValLysleuThrSerTyrgAsprgylValArgSerLysleuGluSerTyrg 313
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Db 841 AGGATGCCCAATTTGATGCTGATGCTGCTAA----- 870
Qy 334 LysProLeuTyrgLysProHisTyrgValArgAlaHisGluArgLysleuAlaLeuAspVal 353
Db 871 GAAGGCTCTATCT-----CAACTGTCCAAATGAGACTGT 903
Qy 354 LeuSerValSerIleAspSerThrProLysGlnSerLysAsnSerAspMetValMetThr 373
Db 904 TTTCACATG-----CATCATATTTCCAGAGCATCTCCACAGCTAGCCCA 948
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Qy 394 MetIleArg-----ProValAsnIleSerGlyPheAspPhePro 406
Db 1003 AGAATATAAATCTTTGTGCACCTATGTGAATGATTAATTTGAGACATTTGAC----- 1056
Qy 407 AlaAspValAspMetTyrgValArgIleGluPheSerValTyrgValGlyThrLeuThrLeu 426
Db 1057 -----AAGTATTATGTTGACAA-----GGATCTACCATGAGAGAACCTTA 1101
Qy 427 AlaSerLys-----SerThrThrLysValAlaAsnAlaGlnPheAlaLysTrpAsnLysGluMet 445
Db 1102 TGTGATTAATGTGAACCTCAAGAGTACCTTGTTCATCCAGCTGAGTAT---GAATGG 1158

Qy 446 TyrThrPheAspLeuTyrgMetLysAspMetProProSerAla-----ValLeuSerIle 463
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Db 1219 TGTTCGTAAAGCGCAAGAGGCTGTAAGAGAACCTGCTCCATCTGCGCTGGGGAAT 1278
Qy 484 MetSerLeuThrAspTrpArgAsprglnLeuArgGlnGlyGlnPheLeuPheHisLeuTrp 503
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Qy 524 Asn-----AlaAlaValThrIleGluIleSerSerTyrgLysArgVal 538
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Qy 539 ArgMetProSerGlnGlyGlnTyrgThrTyrgLeuValLysHisArgSerThrTrpThrGlu 558
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Qy 559 Thr-----LeuAsnIleMetGlyAspAsp 566
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Qy 567 TyrgLys-----SerCysIleArgAspProGly 575
Db 1561 AATGAATTAAGAAATATGATTAAGAACAGCTCCGAGCAATTTGTACACGAGATCTCTGA 1620
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Qy 713 ArgIleGlyHisArgLeuPheThrPheLeuArgAlaGluIleAlaArgLeuArgAspCys 732
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 924 ArgSerIleAspProSerPheMetAsnLysIleIyLysGlnCysGlyIleGluAsp 943
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 1124 TyrGlnGlnAlaPheAsnGlySerThrSerThrLysThrAsnThrLeuPheHisAlaVal 1143

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 RESULT 5
 US-08-162-081B-34
 Sequence 34, Application US/08162081B
 Patent No. 5624492
 GENERAL INFORMATION:
 APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter
 APPLICANT: Joseph, Otau, Masayuki; Panayotou, George; Volinia,
 APPLICANT: Stefano, Gout, Ivan Tarasovitch
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,081B
 FILING DATE: February 7, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-162-081B-34
 Alignment Scores:
 Pred. No.: 7,16e-119 Length: 3240
 Score: 1082.00 Matches: 309
 Percent Similarity: 47.13% Conservative: 225
 Best Local Similarity: 27.27% Mismatches: 437
 Query Match: 17.90% Indels: 162
 DB: 1 Gaps: 39
 US-08-908-453-1 (1-1146) x US-08-162-081B-34 (1-3240)
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 Qy 225 GlnMetPheTrp-----ArgLysArgIleValIleGlu 235
 Db 574 GTGTGATTTGGTAAATAGTTTCTCCAAATTAATGACACAGAGAAATATCTGTGAATATC 633
 Qy 236 AsnGlyValCys-----GluLysMetMetLysIleGlnIleGluPheAsnProAsnGlu 253
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 Qy 254 ThrProLysSerIleuHisThrPheLeuTyrglnMetCArgLysLeuAspValTyra 273
 Db 685 ACTAGAAAGTATGTGCTATCATCT-----GAACATTAATAACTGTGTGTTTAGAA 735
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 Qy 333 ProLysProLeuTyrglnProHisTyrglnAlaArgIleGluArgLysLeuAlaLeuAsp 352
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 Qy 373 ThrAspPheArgProThrIleAspSerLysGlnValSerIleuTrpAspLeuAspAlaAsn 392
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 Qy 606 Tyr-----IleGlnLysGlnIleProAspLeuLeuIleValLeuSerGluLeuAla 622
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 Qy 663 ArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerProValThrPheHisLeuPhe 682
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 Qy 683 IleLeuProLeuIleGlnAlaLeuLysTyrglnProArgAlaGlnSerGluValGlyMet 702
 Db 1894 TTAATTCAGCTATGTACAGGCTCTTAATATATGAAACAATTTTGGATTAACCTGTGTGAGA 1953
 Qy 703 MetLeuLeuThrArgAlaLeuCysAspTyrglnIleGlyHisArgLeuPheTrpLeuLeu 722
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 Qy 722 ArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrglnArgIle 742
 Db 2014 AAATCTGAGATGCAC-----AATTAACAGTTAGCCAGAGGTTT 2052
 Qy 743 SerLeuLeuMetGluAlaTyrglnArgGlyAsnGluGlnHisIleLysIleIleThrArg 762
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 Qy 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsn 802
 Db 2173 GAT---GAAACCAAAAGGTA-----CAGATGAAGTTTATGTTGACCAATATGAGCGCA 2223

[illegible]

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US-08-780-872-34
; Sequence 34, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinla,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/SB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ. ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-872-34

Alignment Scores:
Pred. No.:
Score: 7.16e-119 Length: 3240
Percent Similarity: 1082.00 Matches: 309
Best Local Similarity: 47.13% Conservative: 225
Query Match: 27.27% Mismatches: 437
QB: 17.90% Indels: 162
Gaps: 39

US-08-508-453-1 (1-1146) x US-08-780-872-34 (1-3240)
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QY 108 GLYGLILIGLIVALLIIEPHEANAPARGLINPROLEUSERLYVLEUGILYUENIGLY 127
DB 229 GCAGAAAGGAAAGAAATTTTGTATGAAACAAAGACGACTTGTGATCTTCGGCTTTTCAA 288
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Db      2344 AATTGGAGAACCCAGACATCATGTCCAGGTTACTGTTCCAGAACCAATAGATCATCTTT 2403
Qy      854 LysAsnGlyAspAspLeuArgLysAspMetLeuValIleuValIleuValMetAsp 873
Db      2404 AAAAATGGGGATGATTACGGCAAGATATGTAACCTTCAAATATTGTTATGTA 2463
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Db      2464 AATATCTGGCAAAATCAAGGTCTGATCTTCAGATGTACCTTATGTTGTGTGCAATC 2523
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Qy      914 ValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPheMetAsnLys 933
Db      2584 TGCAAAGGGGCTTGAAAGGTGCACG-----CAGTTCAACAGCCACACTACATCAG 2637
Qy      934 TrpIleAspGlySerGlyIleGluAspGlyLysLysSerLysLysAspSerThr 953
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Qy      954 LysAsnProIleGlyLysLysIleAspAsnThrGlnAlaMetLysLysTyrPheGluSer 973
Db      2656 AAGAGGAATAT-----TATATGACAGCC 2679
Qy      974 ValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIleMetGlyIle 993
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Db      3040 CAATCTTTTGGATGATTCATTCATCACTGCAAAAGACCTTACCTTATGAT---AAACTGAG 3096
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APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
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Alignment Scores:
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Db 2404 AAAAATGGGAGATTTTACGGACAGATATGCTAACCTTCAATATTCGTTATGGA 2463
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Qy 1014 PheGlyHisIleLeuGlyHisIleGlyLysThrLysLeuGlyIleGlnArgAspArgLysPro 1033
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RESULT 8

US-08-162-081B-32

Sequence 32, Application US/08162081B

Patent No. 5824492

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu

APPLICANT: Bala, Waterfield, Michael Derek, Parker, Peter

APPLICANT: Joseph, Otsu, Masayuki, Panayotou, George, Volinia,

APPLICANT: Stefano, Gout, Ivan Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

TITLE OF INVENTION: THEIR PREPARATION AND USE

```

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"
US-08-162-081B-32
Alignment Scores:
Pred. No.: 1.8e-118 Length: 3412
Score: 1079.00 Matches: 308
Percent Similarity: 47.13% Conserved: 226
Best Local Similarity: 27.18% Mismatches: 437
Query Match: 17.85% Indels: 162
Gaps: 39
US-08-908-453-1 (1-1146) x US-08-162-081B-32 (1-3412)
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Qy 90 GlyThrTyrSerValLysProGlnAsp-----TyrValPheArgGlnLeuAsnAsnPhe 107
Db 169 CCTCTCCATCAACTCTTCAAGATGAATGATCTTCAATTTTCTGTAAGTTTAAACCAAGA 228
Qy 108 GlyIleGluValIlePheAsnAspAspGlnProLeuSerLysLeuGluLeuHisIleGly 127
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Qy 148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGluGluSerLeuAspGlu 167
Db 343 CGAGAAATTTGTTTGTGATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCT 402
Qy 168 GlnLeuArgGlnPheArgAlaSerLeuTrpAlaArgThrLysLysThrCysLeuThrArg 187
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Db 463 GATCTTAATTCACCTCATATGATGACAAATGATGCTATCCG-----CCACATGTAGAA 516
QY 205 ValGlyGlySerCysProLysAspLeuGlySerLysValLysAlaAlaLysLeuSerTyr 224
Db 517 TCTTACCAGACGACTGCCAAGACATATATATTAATGTGATAGAGCCAAATA---ATA 573
QY 225 GluMetPheTrp-----ArgLysArgLysAlaGluLe 235
Db 574 GTGGGATTTGGGTATATAGTCTTCTCCAAATAATGACMACAGAAAGATATCTGTGAAATAC 633
QY 236 AsnGlyValCys-----GluLysMetMetLysIleGluIleGluPheAsnProAsnGlu 253
Db 634 AACCATGACTGTGTGCCAGACACAGTAATGTGTAAGCAATCAG-----AAAAA 684
QY 254 ThrProLysSerLeuLeuHisThrPheLeuTyrGluMetArgLysLeuAspValTyrAsp 273
Db 685 ACTAGAAATGATGTGCTATCATCT-----GAACATATAAACTGTGTGTTTAGAA 735
QY 274 ThrAspAspProAlaAspGluGlyTrpPheLeuGluLeuAlaGlyArgThrThrPheVal 293
Db 736 TATCAGGGCAG-----TACATTTTAAAGTGTGTGATGTGATGATAATCTTC 783
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QY 373 ThrAspPheArgProThrAlaSerLeuLysGlnValSerLeuTyrAspLeuAspAlaAsn 392
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QY 703 MetLeuLeuThrArgAlaLeuLysCysAspTyrArgIleGlyHisArgLeuPheTrpLeuLeu 722
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 RESULT 9
 US-08-780-872-32
 ; Sequence 32, Application US/08780872
 ; Patent No. 5846824
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano, Gout, Ivan Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Felte & Lynch
 ; STREET: 805 Third Avenue

CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/780, 872
 FILING DATE: 09-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/162, 081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEO ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3412 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single or double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3204
 OTHER INFORMATION: /standard_name="CDS"
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 Alignment Scores:
 Pred. No.: 1,86-118 Length: 3412
 Score: 1079.00 Matches: 308
 Percent Similarity: 47.13% Conservative: 226
 Best Local Similarity: 27.18% Mismatches: 437
 Query Match: 17.85% Indels: 162
 DB: 2 Gaps: 39
 US-08-908-453-1 (1-1146) x US-08-780-872-32 (1-3412)
 Qy 70 GluileLysLeuSerAspPheLysHisGlnLeuPheGluLeuIleAlaPrometLysTrp 89
 Db 115 GAGGCTACATTAAGTAACTATAAAGCATGACATTTTAA-----GAAGCAAGAAATATC 168
 Qy 90 GlyIleTyrSerValLysProGlnAsp-----TyrValPheArgGlnLeuAsnAsnPhe 107
 Db 169 CCTCTCCATCAACTCTTCAAGATGAATCTTCTTACATTTTCGTAAAGTGTACCCAGAA 228
 Qy 108 GlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLysLeuGluLeuHisGly 127
 Db 229 GCAGAAAGGAAAGATTTTGTGATGAACAAGACGACTTGTGATCTTCGGCTTTTCA 288
 Qy 128 ThrPhePrometLeuPheLeuTyrGlnProAspGlyIleAsnArgAspLysGluLeuMet 147
 Db 289 -----CATTTTAAAGTAAATGACACAGAGCAACCGGAAAGAAATCTTCAT 342
 Qy 148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGluGluSerLeuAspGlu 167
 Db 343 CGAGAAATGTTTGTTCATGCGCATGCGCATGCGCAATTTGAATGATTAAAGATCTCT 402
 Qy 168 GluLeuArgGlnPheArgAlaSerLeuTrpAlaGlnThrLysLysThrCysLeuThrArg 187
 Db 403 GAAGTACGAGACTTCGAAAGAAATATTTCTTAATGTTTAAAGAAAGCTGTGATCTTAGG 462
 Qy 188 GlyLeu-----GluGlyThrSerHisIleTyrAlaPheProGluGluGlnTyrLeuCys 204

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Db      463 GATCTTAATCACTCATAGTAGAGCAATGTATGTCTATCCG-----CCACATGTAGAA 516
Qy      205 VALGlyGlySerCysProlysaAspleuGlySerLysValIlysaAlaIlyleuSerTyr 224
Db      517 TCTTCACCGAGAGCTGCCAAGACATATATTAATTTGATAGAGGCCAAATA--ATA 573
Qy      225 GluMetPheTyr-----ArgLysArgLysAlaGluIle 235
Db      574 GTGGTGATTTGGGTAAATAGTTCTTCCAAATTAATGACAGACAGAGATATCTCTGAAAAATC 633
Qy      236 AsnGlyValCys-----GlyLysMetCysIleGluIleGluPheAsnProAsnGlu 253
Db      634 AACCATGACGTGTGCCAGAACAGATATGCTGAGCAATCAGG-----AAAAA 684
Qy      254 ThrProLysSerLeuLeuHisThrPheLeuTyrGluMetArgLysLeuAspValTyrAsp 273
Db      685 ACTAGAGATGTGTCTATCATCT-----GAACCAATTAACCTGTGTGTTTGAAGA 735
Qy      274 ThrAspAspProAlaAspGluGlyTyrPheLeuGluLeuAlaGlyArgThrThrPheVal 293
Db      736 TATCAGGGCAGG-----TACATTTTAAAGTGTCGTGATGATGATGAAATCTTC 783
Qy      294 ThrAsnProAspValIlyleuThrSerTyrAspGlyValArgSerGluLeuGlySerTyr 313
Db      784 CTAGAA---AAATATCCTCTGAGTCAGTAAAGTATATAGAAAGCTGTATATGCTTGGG 840
Qy      314 ArgCysProGlyPhe---ValValArgArgGlnSerLeuValLeuLysAspTyrCysArg 332
Db      841 AGCATGCCCAATTTGAAGATGATGAGCTTAAGAAAGCCCTTAT----- 882
Qy      333 ProLysProLeuTyrGluProHisTyrValArgAlaHisGluArgLysLeuAlaLeuAsp 352
Db      883 -----TCTCAACTGCCCAATGAGC 900
Qy      353 ValLeuSerValSerIleAspSerThrProLysGlnSerLysAsnSerAspMetValMet 372
Db      901 TGTATTTCATG-----CCATCTTATTCACAGCGCATTCACACAGCTTACA 945
Qy      373 ThrAspPheArgProThrAlaSerLeuLysGlnValSerLeuThrAspLeuAspAlaAsn 392
Db      946 CCATATATGATGAGAGAAACATCTACAAA-----TCCCTTGGGTTTAAATATAGACA 999
Qy      393 LeuMetIleArg-----ProValAsnIleSerGlyPheAspPhe 405
Db      1000 CTCAGAAATAAAATTTCTTGTGCACTACGTACGTAAATTTTGAGACATTCG--- 1056
Qy      406 ProAlaAspValAspMetTyrValArgIleGluPheSerValTyrValGlyThrLeuThr 425
Db      1057 -----AAGATTATATGTTGCAACA-----GGTATCTACCATGAGAGGAAACCC 1098
Qy      426 LeuAlaSerLys---SerThrThrLysValAsnAlaGlnPheAlaLysThrPheLysGlu 444
Db      1099 TTATGTGACANGTGACACTCAAGAGATCACTTGTTCACATCCCAAGTGGAAAT---GAA 1155
Qy      445 MetTyrThrPheAspLeuTyrMetLysAspMetProPheSerAla-----ValLeuSer 462
Db      1156 TGCGCTGAATTTATGATATATCATCTCTGATCTCTCTCGTCTCTGACATTCCTCTTC 1215
Qy      463 IleArgValLeuTyrGlyLysValIlyleuLysSerGluGluPheGluValGlyTyrPheVal 482
Db      1216 ATTGTCTCTGTAAAGCGCGAAAGGGTGTAAAGAGACACATGTCATTCATGCGATGGGGA 1275
Qy      483 AsnMetSerLeuThrAspThrAspArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeu 502
Db      1276 AATATAAATCTGTTTATTAACACAGACACTCTAGTATCTGGAAAAATGCGTTGAATCTT 1335
Qy      503 TrpAlaProGluProThrAlaAsnArgSerArgIleGlyLysAsnGlyAlaArgIleGly 522
Db      1336 TGG---CCAGTACTCATGATATAGAAAGATTTCGTGAAACCCATTTGTGT---ACTGGA 1389
Qy      523 ThrAsn-----AlaAlaValThrIleGluIleSerSerTyrGlyLysArg 537
Db      1390 TCAAAATCCAAATTAAGAAATCTCATGCTTAGAGTTGAGTTGACTGTTCACAGCTGTG 1449

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Qy      538 ValArgMetProSerGlnGlyGlnThrTyrThrLysValLysArgSerThrThrThr 557
Db      1450 GTAAAGTTCCAGATATGTCA-----GTATTAAGACATGCCAATTTGGTCT 1497
Qy      558 GluThr-----LeuAsnIleMetGlyAsp 565
Db      1498 GTATCCCGAAGACAGATTTAGCTATTCACCGCAGGACTGATGATACAGACTACTGAA 1557
Qy      566 AspTyrGlySerCysIleArgAspProGlyTyrLysLysLeuGluMetLeuValLysLys 585
Db      1558 GACAAATGAA-----TTAAGGAAATATGACAAAGACAGCTCAAAATTTCTACACA 1611
Qy      586 HisGluSerGlyIleValLeuGluLysAspGluGlnArgHisValThrMetThrArg 605
Db      1612 GATCTCTCTCTGAAATCACTGAGCAG---GAGAAAGATTTTCTATGAGATCAGACAGAC 1668
Qy      606 Tyr-----IleGlnLysGlnLysProAspLeuLeuIleValLeuSerGluLeuAla 622
Db      1669 TATGTGTAACTATCCCGAAATTTCTACCAATTTGCTT-----CTGTCT 1713
Qy      623 PheValIleThrThrAspArgGluLysAsnPheSerGluLeuTyrValMetLeuGluLysThrPys 642
Db      1714 GTTAAATGGAATTTCTAGAGATCAAGTACCCAGATGTATGCTTGTGTAAGATTTGGCCT 1773
Qy      643 ProPheSerValAlaAlaAlaLeuThrLeuLeuGlyLysArgCysThrAspArgValIle 662
Db      1774 CCATCAAACTGAAACAGGCTATGGAACCTTCTGACCTGTAATTCACCAATCTTATGCTT 1833
Qy      663 ArgLysPheAlaValAlaGluLysLeuAsnGluLeuSerProValThrPheHisLeuPhe 682
Db      1834 CGAGGTTTGTCTGTCGGTGCTGGAATAATTTATACAGATGACAAATCTTCTCAGTAT 1893
Qy      683 IleLeuProLeuIleGlnAlaLeuLysTyrGluProAlaArgAlaGlnSerGluValGlyMet 702
Db      1894 TTAATTCAGTATGACAGTCTCTAAATATGAAACATATTTGGATTAATCTGCTTGTGAGA 1953
Qy      703 MetLeuLeuThrArgAlaLeuLysCysAspTyrArgIleGlyHisArgLeuPheThrLeuLeu 722
Db      1954 TTTTATCTGAGAAAGACATTTACTATCAAAAGATTTGGCACTTTTCTTTGGCATTTA 2013
Qy      723 ArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrArgArgIle 742
Db      2014 AATATGATGATCAC-----AATAAACAGTTAGCAGAGGTTT 2052
Qy      743 SerLeuLeuMetGluAlaTyrLeuArgGlyAsnGluGluHisIleLysIleLeuThrArg 762
Db      2053 GGCCTGCTTTGGAGTCTTATTTGTGTCGATGTCGATGATGATTTTGAAGACACTGAAATAG 2112
Qy      763 GlnValAspMetValAspGluLeuThrArgIleSerThrLeuValIlyleGlyMetProLys 782
Db      2113 CAAGTCGAGCAATGGAAGAGCTCATTTAACTTAACGTACATTTCTCAACAGAGAGGAAAG 2172
Qy      783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluLysn 802
Db      2173 GAT---GAAACACAAAGGTA-----CAGATGAAGTTTATTGAGCAAAATGAGGCGA 2223
Qy      803 MetAsp-----SerProLeuAspProValTyrLysLeu 813
Db      2224 CCAAGATTTCAATGATGCCCTTACAGGCTTGTCTCTCTTAAACCTGCTCATACACTA 2283
Qy      814 GlyGluMetIleIleAspLysAlaIleValLeuGlySerAlaLysArgProLeuMetLeu 833
Db      2284 GGAACCTAGGCTTAAAGAGTGTGAATATATGCTTCTTGCAAAAAGCCACTGTGCTTG 2343
Qy      834 HisTrpLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIlePhe 853
Db      2344 AATGGGAGAACCCAGACATCATGTCAAGATTACTGTTTCAAGAACATAGATCATCTTT 2403
Qy      854 LysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGluValMetAsp 873
Db      2404 AAAAATGGGAGATTTATGCGCAAGATATGCTTACCACTTCAATATTTCTGATTTATGGA 2463

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Qy 874 AenietrlysalalaleamileaspCyseleasnpProTyralaValleuprowec 893
Db 2464 AATATCTGGCAAAATCAAGGCTTGTATCTTCGAATGTTACCTTATGCTGTCTGCAATC 2523
Qy 894 GlyglumetilegyllelleleluvalProasncyselythrillephegluilegin 913
Db 2524 GGATGCTGGTGGCACTTATGAGGTGGCCAAATCTCACACTTATTCGCAAAATTCAG 2583
Qy 914 ValglythrGlyPheMetasnthralaValargserileaspProserPheMetasnth 933
Db 2584 TGCAAAAGCGGCTTGAAAGGTGCACTG-----CACTTCACAGCCACACACTACATCAG 2637
Qy 934 Trrilearglyglncyselylleleluaspglulyslylseserlylsaspsertthr 953
Db 2638 TCGCTC-----AAAACACAGAAC 2655
Qy 954 LyasapnProilleglulysleleaspanthrGlnalMetlylselyrPhegluser 973
Db 2656 AAAGAGAAAT-----TATGATGACGCC 2679
Qy 974 ValasparGpHeuTySerCyseValglyrserValaThrTyrlleMetGlyle 993
Db 2680 ATTGACCTGTTACACGCTTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2739
Qy 994 LysasparGHisSerAspAsnleuMetleuthrGluaspGlylyserTyralHisleasp 1013
Db 2740 GGAGATCGTCACAAATAGTAACATCATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2799
Qy 1014 PhegllyHisleleuglyHislelythrlylsleuglylleGlnargAsparGlnPro 1033
Db 2800 TTTGACACTTTTGGATCACAAGAAAGAAATTTGTTATTAAGAAAGAGAGAGAGAGAGAG 2859
Qy 1034 PheilleuThrGlnHisPheMetThrValleargserlylsaspsertThrValle 1053
Db 2860 TTTGTTTGACACAGGATTTCTTAATAGTATTAGTAAAGAGAGAGAGAGAGAGAGAGAG 2919
Qy 1054 SerHisgluleuGlnlyPhePhePhePhePhePhePhePhePhePhePhePhePhe 1073
Db 2920 ACAAGAGATTTGAGAGGTTTTCAGAGAGAGGTTTTCAGAGAGGTTTTCAGAGAGGTTT 2979
Qy 1074 AsnaArgAspLeuPheValSerleuPheThrleuMetleuglyMetGlnleuProGlu 1093
Db 2980 CATGCCAATCTCTCATTAATCTTTCTCAATGATGCTGGCTGCAATGCCAGAGACTA 3039
Qy 1094 SerThrlysalasPheAspHisleuPhePhePhePhePhePhePhePhePhePhe 1113
Db 3040 CAATCTTTGATGACATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 3096
Qy 1114 GluGluAlaArglyPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 1133
Db 3097 CAAGAGGCTTGGAGTATTTCTAGAAACAAATGATGATGATGATGATGATGATGATGAT 3156
Qy 1134 ThrlyserThrAsnTrpLeuPheHisAlaVallyshistyr 1146
Db 3157 ACAAAATGATGATGATCTTCCACACAAATTAACAGCAT 3195

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RESULT 10
US-09-085-957-32
Sequence 32, Application US/09085957

GENERAL INFORMATION:
PATENT NO. 6274327
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovich
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York

```

/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/085,957
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/780, 872
/ FILING DATE: 09-JAN-1997
/ APPLICATION NUMBER: 08/162, 081
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: PCT/GB93/00761
/ FILING DATE: 13 April 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pasqualini, Patricia A.
/ REGISTRATION NUMBER: 34,894
/ REFERENCE/DOCKET NUMBER: L0D 5256
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEO ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3412 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single or double
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3204
/ OTHER INFORMATION: /standard_name="CDS"
/ US-09-085-957-32
/
Alignment Scores:
Pred. No.: 1,86-118 Length: 3412
Score: 1079.00 Matches: 308
Percent Similarity: 47.13% Conservative: 226
Best Local Similarity: 27.18% Mismatches: 437
Query Match: 17.85% Indels: 162
DB: 4 Gaps: 39
/
US-08-908-453-1 (1-1146) x US-09-085-957-32 (1-3412)
Qy 70 GluilelyleuSerAspPhePhePhePhePhePhePhePhePhePhePhePhePhe 89
Db 115 GAGGCTACATTAAGTAAAGCATGACTATTAA-----GAGGCAAGAAATATC 168
Qy 90 GlyThrTySerVallyPheProGlnasp-----TyValPheArgGlnleuAsnAsp 107
Db 169 CCTCTCCATCAACTCTTCAAGATGAATCTTCTTACATTTCTGTAAGTTCACCAAGNA 228
Qy 108 GlyGluileGluVallePheAsnAspAspGlnProleuSerlyleuGlnleuHisGly 127
Db 229 GCGAAGAGGAAGATTTTGTGATGAACAAGACGACTTGTGATCTTCGGCTTTTCA 288
Qy 128 ThrPhePheMetleuPhePhePhePhePhePhePhePhePhePhePhePhePhe 147
Db 289 -----CATTTTAAAGTAAATTAACCAAGTACCGGAAAGAAAGATCTTCAT 342
Qy 148 SerAspHisSerHisCysleuglyTyserleuAspLyseleuGlnleuSerleuAspGlu 167
Db 343 CGAGAAATGTTTGTGATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCAT 402
Qy 168 GluLeuArgGlnPheArgAlaSerleuThrPheAlaThrlyleuThrCysleuThrArg 187
Db 403 GAGTACGAGACTTCGAGAAATATTTCTTAATGTTTAAAGAGAGCTGTGATCTTAAG 462
Qy 188 Glyleu-----GluGlyThrSerHisTyralaPheProGluGluGlnTyreucys 204

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Db 463 GATCTTAATACCTCATAGTAGAGCAATGTATGTCTATCCG-----CCACATGTAGAA 516
Qy 205 ValGlyUserCysProIysAspLeuGlyUserLysValAlaAlaLysLeuSerTyr 224
Db 517 TCTTCACACGAGCTGTCGCAAGACATATTAATAATGTAGAGGCCAAATA---ATA 573
Qy 225 GluMetPheTyr-----ArgLysArgLysLagLile 235
Db 574 GTGGATGTTGGGTAAATAGTCTTCCAAATAATGACAGACAGAAAGTATCTCTGAAATATC 633
Qy 236 AsnGlyValCys-----GluLysMetLysLileGluLysPheAsnProAsnGlu 253
Db 634 AACCATGACTGTGTGCACAAACAGATTAATGTGCAAGCAATCAGC-----AAAAA 684
Qy 254 ThrProLysSerLeuLeuHisThrPheLeuTyrGluMetArgLysLeuAspValTyrAsp 273
Db 685 ACTAGAAATGTGTGTATCATCT-----GAACAATTAATAACTGTGTGTTTAGAA 735
Qy 274 ThrAspAspProAlaAspGluGlyTyrPheLeuGluLeuAlaGlyArgThrPheVal 293
Db 736 TATCAGGGCAAG-----TACATTTTAAAGTGTGTGATGTGATGATGATATCTTC 783
Qy 294 ThrAsnProAspValLysLeuThrSerTyrAspGlyValArgSerGluLeuGlyUserTyr 313
Db 784 CTAGAA---AAATATCTCTGAGTCACTAATAGTATATAGAAAGCTGTATATGCTTGGG 840
Qy 314 ArgCysProGlyPhe---ValValArgArgGlnSerLeuValLeuLysAspTyrCysArg 332
Db 841 AGCATGCCCCAATTGGAAGATGATGGCTTAAGAAAGCCCTTAT----- 882
Qy 333 ProLysProLeuTyrGluProHisTyrValArgAlaHisGluArgLysLeuAlaLeuAsp 352
Db 883 -----TCTCAACTGCCAATGGAC 900
Qy 353 ValLeuSerValSerLileAspSerThrProLysGlnSerLysAsnSerAspMetValMet 372
Db 901 TGTATTACATG-----CCATCTTATTCAGACGCAATTCACACAGCTACA 945
Qy 373 ThrAspPheArgProThrAlaSerLeuLysGlnValSerLeuTyrAspLeuAspAlaAsn 392
Db 946 CCATATATGATGAGAGAAACATCTACAAA-----TCCCTTGGGTTTAAATAGAGCA 999
Qy 393 LeuMetLileArg-----ProValAsnLileSerGlyPheAspPhe 405
Db 1000 CTCAGAAATAAAATTTCTTGTGCAACCTACGTGATCTTAATTTTGACAACATGAC--- 1056
Qy 406 ProAlaAspValAspMetTyrValArgLileGluPheSerValTyrValGlyThrLeuThr 425
Db 1057 -----AAGATTATGTTCGAAACA-----GGTATCTACCATGAGAGAAACCC 1098
Qy 426 LeuAlaSerLys-----SerThrLysValAsnAlaGlnPheAlaLysTyrPheLysGlu 444
Db 1099 TTAATGACAAATGTCACACTCAAAAGATACCTTGTTCACATCCACAGGTGAT---GAA 1155
Qy 445 MetTyrThrPheAspLeuTyrMetLysAspMetProProSerAla-----ValLeuSer 462
Db 1156 TGGCTGAATTTATATATATATATATCTCTGATCTTCTCGCTGCTGCACTTGGCTTTC 1215
Qy 463 LileArgValLeuTyrGlyLysValLysLysLeuLysSerGluLysPheGluValGlyTyrVal 482
Db 1216 ATTGCTCTGTAAAGCGCAAGGCTGCTAAAGAGAGAACACTGTCATCGATGGCATGGGA 1275
Qy 483 AsnMetSerLeuThrAspTyrPheArgAspGluLeuArgGlnGlyLysPheLeuPheHisLeu 502
Db 1276 AATATAACTTGTTAATTAACACAGACACTTAGTATCTGAAAAATGCTTGAATCTT 1335
Qy 503 TTPAlaProGluProThrAlaAsnArgSerArgLileGlyLysAsnGlyAlaArgLileGly 522
Db 1336 TGG---CCAGTACTCATGATTAGAAGATTTGCTGCAACCTATGTGT---ACTGCA 1389
Qy 523 ThrAsn-----AlaAlaValThrLileGluLileSerSerTyrGlyLysArg 537
Db 1390 TCAAAATCAAAATTAAGAAATCTCATGCTTAGAGTTGAGTTTGACTGTTCACACAGTGG 1449

Qy 538 ValArgMetProSerGlnGlyGlnTyrThrTyrLeuValLysHisArgSerThrThrThr 557
Db 1450 GTAAGTTTCCAGATATGTCA-----GTGATTGAAGACATGCCAATTTGCTCT 1497
Qy 558 GluThr-----LeuAsnLileMetCylAsp 565
Db 1498 GTATCCGAGAGACAGATTTAGCATTTCCACGACGAGACTGATPAACAGACTAGCTAGA 1557
Qy 566 AspTyrGlyUserCysLileArgAspProGlyTyrTyrLysLysLeuGluMetLeuValLysLys 585
Db 1558 GACAAATGAA-----TTAAGGAAATGACAAAGAACGCTCAAGCAATTTCTACACGA 1611
Qy 586 HisGlyUserGlyLileValLeuGluLysAspGluGlnArgHisValTyrMetTyrArgArg 605
Db 1612 GATCTCTCTCTGAATACCTGAGCG---GAGAAAGATTTTCTATGAGATCACAGACAC 1668
Qy 606 Tyr-----LileGlnLysGlnGluProAspLeuLileValLeuSerGluLeuAla 622
Db 1669 TATTGTGATCATTCGCCGAATTTCTACCAATTTGCTT-----CTGTCT 1713
Qy 623 PheValTyrThrAspArgGluAsnPheSerGluLeuTyrValMetLeuGluLysTyrLys 642
Db 1714 GTTAATGGAATTTCTAGAGATGAACTAGCCAGATGATTTGCTGTAAAGATTGGCCT 1773
Qy 643 ProProSerValAlaAlaLileuThrLeuLeuGlyLysArgCysThrAspArgValLile 662
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Qy 663 ArgLysPheAlaValAlaGluLysLeuAsnGluLysLeuSerProValThrPheHisLeuPhe 682
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Db 1894 TTAATTCAGCTAGTACAGTCTCTAAATAATGAAACATTTGGATTAATCTTGTGTGAGA 1953
Qy 703 MetLeuLeuThrArgAlaLeuLysCysAspTyrArgLileGlyHisArgLeuPheTyrLeuLeu 722
Db 1954 TTTTACTGAGAAAGCATTTGACTTAATCAAAAGATTTGGCACTTTTCTTTTGGCATTTA 2013
Qy 723 ArgAlaGluLileAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrArgArgLile 742
Db 2014 AATATCGATGATCAC-----AATAAACAGTTAGCCAGAGCTT 2052
Qy 743 SerLeuLeuMetGluAlaTyrLeuArgGlyAsnGluGluHisLileLysLileLeuThrArg 762
Db 2053 GGCCTGCTTTTGGAGTCTTATTTGTGTCATGTGATGTATTTGAACACCTGAAATAGG 2112
Qy 763 GluValAspMetValAspGluLeuThrArgLileSerThrLeuValLysGlyMetProLys 782
Db 2113 CAAGTCGAGCAATGAAAGCTCATTTAACTTAATGACATTTCTCAAAACAGAGAGAGAG 2172
Qy 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerLileSerHisLysMetGluAsn 802
Db 2173 GAT---GAAACCAAAAGSTA-----CAGATGAAGTTTGTAGAGCAATTAGAGCGCA 2223
Qy 803 MetAsp-----SerProLeuAspProValTyrLysLeu 813
Db 2224 CCAGATTTTCATGATGCCCTACAGGCTTGCTGTCTCTTAACCTGTGCTCATCACTA 2283
Qy 814 GlyLysMetLileLileAspLysAlaLileValLeuGlySerAlaLysArgProLeuMetLeu 833
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Qy 834 HisTyrLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetLilePhe 853
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Qy 854 LysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGluValMetAsp 873
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Qy 874 AeniletrpLysalaalaalaenileapCysCysleuAsnProTyrAlaValleuProMet 893
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Qy 934 TrpIleArgLysGlnCysGlyIleGluAspGluLysLysSerLysAspSerThr 953
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Db 2740 GGAAGATCGTCACAAATAGTAACATCATGCGTGAAGAACGATGCAACATGTTTCAATAGAT 2799
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Db 2800 TTTGGACACTTTTGGATGACAAAGAAAGAAATTTGTTAATAAGAACGATGCGCA 2859
Qy 1034 PheIleLeuThrGlnHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsn 1053
Db 2860 TTTGTTTGACACAGGATTTCTTAATAGATTAGTAAGAGAGCCCAAGATGACAAAG 2919
Qy 1054 SerHisGluLeuGlnLysPheLysThrLeuCysValGluAlaTyrGluValMetTrpAsn 1073
Db 2920 ACAAGAGAAATTTGAGAGGTTTCAAGGATGTTTCAAGGCTTATCTACTTATTCAGACG 2979
Qy 1074 AsnArgAspLeuPheValSerLeuPheThrLeuMetLeuGlyMetGluLeuProGluLeu 1093
Db 2980 CATGCCAATCTCTCATTAATCTTTCTCAATGATGCTTGGCTCGAATGCCAGACATA 3039
Qy 1094 SerThrLysAlaAspLeuAspHisLeuLysThrLeuPheCysAsnLysGluSerLys 1113
Db 3040 CAATCTTTGATGACATTCATGATCAATCGAAAGACCCCTTAGAT--AAACTGAG 3096
Qy 1114 GluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAlaPheAsnLysSerTrpSer 1133
Db 3097 CAAGAGGCTTGGAGATTTCATGAAGCAATGAATGATGACATCATGTGCTGGACACA 3156
Qy 1134 ThrLysThrAsnTrpLeuPheHisAlaValLysHisTyr 1146
Db 3157 ACAAAATGATGATGATCTTCCACACAAATTAACAGCAT 3195

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RESULT 11

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US-08-916-917-3
Sequence 3, Application US/08916917
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkings, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

```

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; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-917-3

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Alignment Scores:
Pred. No.: 1,836-113 Length: 3808
Score: 1038.00 Matches: 316
Percent Similarity: 46.96% Conservative: 224
Best Local Similarity: 27.48% Mismatches: 400
Query Match: 17.17% Indels: 210
DB: Gaps: 46

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US-08-908-453-1 (1-1146) x US-08-916-917-3 (1-3808)

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Qy 68 SerLeuGluIleLysLeuSer--AspPheLysHisGlnLeu-----PheGlu 82
Db 330 GCGCTGGAGACGAGGCTTCTTGAGACTTTCACACCGGTTGCGCCGACCACTTCTC 379
Qy 83 LeuIleAlaProMetLysTrpGlyThrTyrSerValLysProGlnAspTyrValPheArg 102
Db 380 CTGGCTTCCAGAAAGAGGAGTGTCGACGATCTATGACAAAGTACAGAGTGTCAG 439
Qy 103 GlnLeuAsnAsnPheGlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLys 122
Db 440 ACCCTGAGACTGCTCGCTACGAGAGGTTTGACACCGAGCCCGGCGCATTCACGTC 499
Qy 123 LeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArg 142
Db 500 GTCCAGCGGACGCGCCCTCGAGAGACATTCGCTTCAG----- 541
Qy 143 AspLysGluLeuMetSerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGlu 162
Db 542 -----CGCCAGCTCAAGCCTCATGCTGCTACGAGTCACGACGTCAGC 586
Qy 163 GluSerLeuAspGluGluLeuArgGlnPheArgAlaSerLeuTrpAlaArgThrLysLys 182
Db 587 AACGTCATGACGAGAGACTG--GAGTTC-----ACGGGGGCC 622
Qy 183 ThrCysLeuThrArgGlyLeuGluGlyThrSerHisTyrAlaPheProGluGluGlnTyr 202
Db 623 CGCTGCTGAC----- 634
Qy 203 LeuCysValGlyGluSerCysProLysAspLeuGluSerLysValLysAlaLysLeu 222
Db 635 -----CCGCGCATGCGCGGAGTGGCGCGCGGACCCCAAGCTT 673
Qy 223 SerTyrGlnMetPheTrpArgLysArgLys-----AlaGluIle 235

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Db 674 TAGGCATGACCCCTGGGTGACATCCAGACCCCTCTGAGTACCTTGTGAAGAATGC 733
 Qy 236 AanglyValCys-----GluysMetMetLeu1leGln1leGluPhe 249
 Db 734 ACTAACATCTGGCTTTCATCTCATTCACCGACAGACACGACGACCAATCAAGATGC 793
 Qy 250 AasnProAsnGluThrProlysSerLeuLeu1sthrPheLeuTyrlMetArglys--- 268
 Db 794 TCGGCCGATGACACCCGACGACCATCTCCAGAGTTCTTTACCAAGATGGCCAAAG 853
 Qy 269 -----LeuAspValTyraSprthraAspProAlaAspGluTyrlPheLeuGln 285
 Db 854 AATCTCTGATGATATCTCTGAAAGCCAGAACGAGGAC-----TTGTGCTGCCG 907
 Qy 286 LeuAlaGlyArgThrThrPheVal1ThrAsnProAspVal1LeuLeuThrseryrAspGly 305
 Db 908 GTCTGGCGCGGATGATGATCTGTGGGT---GAAACGCCCATCAAAATTTCCAGTGG 964
 Qy 306 ValArgSerGluLeuGluSerTyraGysProGlyPheVal1ValArgGlnSerLeu 325
 Db 965 GTGAGGACGTCTCAAGAT-----GGGAGAGATTCAC-----CTT 1003
 Qy 326 ValLeuLysAspTyrlCysArgProLysProLeuTyrlGluProHisTyrlValArgAlaHis 345
 Db 1004 GTGCTGGAC-----ACTCTCCAGACCCAGCCCTGAGAG-----GTGAGGAAGAA 1051
 Qy 346 GluArgLysLeuAlaLeuAspVal1LeuSerValSer-----1LeaSerThrProLys 363
 Db 1052 GAGTGGCCCGCTGTGATGATCTGACCGAGGATCTACCTACCAAGAGCTGACCAATC 1111
 Qy 364 GlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSerLeuLysGln 383
 Db 1112 CACGGACAGGACCATGAAAGTGTTCACC----- 1141
 Qy 384 ValSerLeuTyraSprleuAspAlaLeuLeuMet1leArgProValAsn1leSerGlyPhe 403
 Db 1142 GTGTCCCTGTGGAGCTGTGACCGCAAGTTCAGGGTCAAA-----ATCAGAGGCAAT 1192
 Qy 404 AspPheProAla-----AspValAspMetTyrlValArg1leGluPheSerValTyrl 420
 Db 1193 GATATCCCTGTCTCTGCCCGGACCGCTGACCTCAAGGTGTGTGTGAGGCAAAATCCAG 1252
 Qy 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThr---LysValAsn1leGlnPheAla 439
 Db 1253 TATGGCAGCAAGTCTTTGCCCAAGAGAAACAGCCCAACCTTCACAGAGAGGAG 1312
 Qy 440 LysTyrAsnLysGluMetTyrlThrPheAspLeuTyrlMetLysAspMetProSerAla 459
 Db 1313 CTCTGGAAAGCTGGGCTT---GAGTTCAGTATTAATCAAAAGACTTACCAAAAGGGCT 1369
 Qy 460 ValLeuSer1leArgValLeuTyrlGlyLys-----Val 470
 Db 1370 CTGCTGAACCTCCAGATCTAAGCTGGCAAGCTCCAGACCTGTGGCAAGCTTGTGA 1429
 Qy 471 LysLeuLysSerGluGluPheGln-----ValGlyTyrVal1AsnMetSer 485
 Db 1430 GAGATCCCAAGTCCCAAGTCCCAAGCAAGCAAGCTCACTGTGATCTAATGCAATTAATG 1489
 Qy 486 LeuThrAspTyrArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeuTyrAlaPro 505
 Db 1490 CTGATAGACCAACGCTTCTCTGCGCATGGGAGATGTGTCTCAAGTGTG----- 1543
 Qy 506 GluProThrAlaAsnArgSerArg1leGlyGln-----AsnGlyAlaArg 520
 Db 1544 -----CAGTTATCCGGGAAGGGGGAAGACCAAGGAGCTTCAATGCCGAAG 1591
 Qy 521 Ile-----GlyThrAsn-----AlaAlaValThr1leGlu1leSer 532
 Db 1592 CTCACGTCGGGAACCAACCCGGAAGCAAGAGACTCAATGCTCAATCTCTTCTGGAC 1651
 Qy 533 SerTyrlGlyArgValArgMetProSerGlnGlyGlnTyrlThrTyrlLeuValLysHis 552
 Db 1652 AATTACTGCAACCCCATAGCTTGGCT-----AAGCAT 1684

Qy 553 ArgSerThrTyrPheGluThrLeuAsn1leMetGlyAspAspTyrlGluSerCysr1leArg 572
 Db 1685 CGG-----CTTACCCCTGACCCCAAGAGGACCGGGTTCGGGACGAATATGCC 1732
 Qy 573 AspProGlyTyrlLysLysLeuGlnMetLeuValLysLysHisGluSerGly1leValLeu 592
 Db 1733 AATCAGCTTCGGAGCAACTGTGAGGCAATCATAGCAGATCCGCTTAACCACTCACA 1792
 Qy 593 GluGluAspGluGlnArgHisValTyrMetTyrArg---ArgTyrlleGlnLysGlnLys 611
 Db 1793 GCTGAAGCAAGAA-----CTGCTTGCAATTTCAATATGAAGGCTGAGAT 1843
 Qy 612 ProAspLeuLeu1leValLeuSerGluLeuAlaPheVal1TyrThrAspArgLysAspPhe 631
 Db 1844 CCCAAAGCTATCTCAACTCTTTAGC---TCGGTGAATGGGAGCAGCAAGAAATTTGTG 1900
 Qy 632 SerGluLeuTyrlValMetLeuGluLys-----TyrLysProProSerVal1Ala 648
 Db 1901 GCCAAACATACCATTTATTTAGCCAAAGGAGGTCTGGATCAGAGTCTTGTGATGG 1960
 Qy 649 AlaLeuThr-----LeuLeuGlyLysArgCysThrAspArgVal1leArgLysPheAla 666
 Db 1961 GGGTTAACCATGACAGCTCTGACTGCAACTTCTGATGAAAGCTGAGAGCCATTGCA 2020
 Qy 667 ValGluLysLeuAsnGluGlnLeuSerProVal1ThrPheHisLeuPhe1leuProLeu 686
 Db 2021 GTCCAAACATGAGAGCTTGAGAGATGATGACGTCTCCAT---TACTGCTTCAGCTG 2077
 Qy 687 1leGlnAlaLeuLysTyrlGluProArgAlaGlnSerGluVal1leGlyMetMetLeuLeuThr 706
 Db 2078 GTCCAGGCTGTGAATTTGAACCATCATGACATGACGCTCCATCCAGATTTCTGTGAAG 2137
 Qy 707 ArgAlaLeuCysAspTyrlArg1leGlyHisArgLeuPheTyrPheLeuArgAlaGlu1le 726
 Db 2138 CGTGTTTAAGAAACAAAGAAATGTGTCACTTGTGTGTGTGTGTGAAGATGATGATT 2197
 Qy 727 AlaArgLeuArgAspCysAspLeuLysSerGluGluTyrlArgArg1leSerLeuLeuMet 746
 Db 2198 GCCCACTGAGG-----CACTATCAGCAAGAGTTTGCAGTATCTCTG 2239
 Qy 747 GluAlaTyrlLeuArgGly---AsnGluGlnHis1leLys1leLeuThrArgGlnValAsp 765
 Db 2240 GAAAGCTTACTGAGGGGCTGGGCGACAGCAGCATCTGCAGACTTCCACAGCAATGCCAA 2299
 Qy 766 MetValAspGluLeuThrArg1leSerThrLeuValLysGlyMetProLys----- 782
 Db 2300 GTAATTTGACATGTTTCAAAAGTCAACATTTGACATTAATGCTCTGTGAAAGATAT 2359
 Qy 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSer1leSerHisLysMetGluAsn 802
 Db 2360 GAGCTTCAGTTC-----CAAGTATTTCCCAATTAAGCAAAAGCTTGAAGAC 2407
 Qy 803 MetAspSer-----ProLeuAspProVal1TyrlLysLeu 813
 Db 2408 CTACAGAAATTTGAATCTCCCAAGAGCTTTAGTTCCTATGATCTGTGAGTGAAGGCC 2467
 Qy 814 GlyLysMet1leLeuAspLysAla1leValLeuGlnSerAlaLysArgProLeuMetLeu 833
 Db 2468 GGGGACCTGTGATGCAAAAGTAAAGTGAAGGAGCTCCCAAGAAAGCCCTGTGGCTT 2527
 Qy 834 HisTyrLysAsnLysAsnProLysSerAspHis1leuProPheCysAlaMet1lePhe 853
 Db 2528 GAGTTTAATGTGCCGATCTTAGCGCT---CTATCAATGAAGAAATTTGAATTTCTTT 2584
 Qy 854 LysAsnGlyAspAspLeuArgGlnAspMetLeuVal1leGlnVal1leGluVal1leMetAsp 873
 Db 2585 AAAACAGGTGAGATCTGGCCCAAGCATGCTTATTAAGATTTCTAGATTCAGATGAGG 2644
 Qy 874 Asn1leTyrLysAlaAlaAsn1leAspCysLysLeuAsnProTyrlAlaValLeuProMet 893
 Db 2645 TCCATTGGAGACCAATCTTGTGATGTGCTCTCCCATATGAGTGTGATTCATCACT 2704


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Db      2765 CAAGACACA---GTGGGCAACACGGGT-----GCCTTAAGATGAGTCTCGAGTCA 2815
Qy      934 TTPileaglyglucylleGlulapglulylslylserylselylsasperthr 953
Db      2816 TGGCTCAAGAAAAATGCGCTTATTGAAGA----- 2845
Qy      954 LysaenProileglulylsleleaspaenthrglnalmetelyselyrphegluser 973
Db      2846 -----AAGTTTACGACAGCT 2860
Qy      974 ValaapargpheleutyserCysValGlyTyrservalalathrtyrilemetGlylle 993
Db      2861 GTGGAGAGATTGTTATTCCTGCGCGCTACTGCTGTCGCAACCTTGCTTCGGAATA 2920
Qy      994 LysaaparghisSerAspaenleumetleuthrglnaapgllylsetyValhisleasp 1013
Db      2921 GCGGACAGACAAATGACAAATTTATGATCTCAGAAACAGAAATCTATTCTATTGAT 2980
Qy      1014 PheglYhisileleuGlYhisglYsThrlysluaglYlleGlnaargsparglnPro 1033
Db      2981 TTGGACACATTCCTGGGAATTCAAAAGTTCTCGGCAATTAAAGAGGGGTCCA 3040
Qy      1034 PheilleuthrgluhiasepewerThrValleargserGlyLysSerValaspGlyasn 1053
Db      3041 TTTGTCTAACCCAGACTTCTGTTGTGATG-----GGGACTTCTGAAAGAAAGACA 3094
Qy      1054 SerhisgluleuGlnlypheleuthrleuGlyserValGlnalathrGlnuValmetrphen 1073
Db      3095 AGTCTACACTTCACAAATTCAGAGATGCTGCGCAAGGCTTACCTTGCTGTAT 3154
Qy      1074 AsnargapleuPheValserleupheThrleumetleuGlymetGlnuProgluLeu 1093
Db      3155 CACACAAACCTACTATCTCTCTTCCATGATGCTGATACACAGAAATGCCCACTTA 3214
Qy      1094 SerThrlysalaspLeuaspHisleuYslysthrlleupheCysasnGlyGluSerlys 1113
Db      3215 ACCACAAAGAAAGATGATGATACATGCGGATGCCCTCACAGTG---GGCAAAAGTGAG 3271
Qy      1114 GlulGlnalarglyphePhelelaelyleTyrglulGlnalaphasnGlyserTrpser 1133
Db      3272 GAGGATGCTAAATAATTTCTTGATCAGATGATGTAAGTTTGACAGACAAAGATGAGCC 3331
Qy      1134 ThrlysthraenthrleuPheHisalaval 1143
Db      3332 GTGCACTTAAGTGTCTTCTACATCTCTGT 3361

RESULT 13
US-08-972-629-3
; Sequence 3, Application US/08972629
; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/972,629
; CLASSIFICATION:

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-629-3

Alignment Scores:
Pred. No.: 1,83e-113 Length: 3808
Score: 1038.00 Matches: 316
Percent Similarity: 46.96% Conservative: 224
Best Local Similarity: 27.48% Mismatches: 400
Query Match: 17.17% Indels: 210
DB: 2 Gaps: 46

US-08-908-453-1 (1-1146) x US-08-972-629-3 (1-3808)
Qy      68 SerleuGlnuileuLysLeuSer---AspPheLysHisGlnLeu-----PheGlu 82
Db      320 GCGCTGAGAGAGAGAGGTTTCTTGGAAGCTTACACCGGCTTCGGCCCGGACCACTTCTC 379
Qy      83 LeuilealaPrometlyTrpGlyThrTyrservalysProGlnaapTrValaPhearg 102
Db      380 CTGGCTTCCAGAAAGAGGGGAGGTGTACGAGATCTATGACAAATACAGGTGTGTGAG 439
Qy      103 GlnleuanaPheglYlGlnlleglValillePheanaParglnProleuSerlys 122
Db      440 ACCCTGACTCCCTCGCTACTGTGAGGTGTGACCCGACCCCGGCGAGATCACCTG 499
Qy      123 LeuGlnleuHisglYthrPhePrometleupheleuthrglnProaspGlylleasnarg 142
Db      500 GTCCAGCGGCGACGGGCCCTCGAGAGAGACATTGGCCTTCGAG----- 541
Qy      143 AsplysgluLeuMetSeraspIleSerHisCysleuGlyTyrsleuaspLysleuGlu 162
Db      542 -----CGCCNAGCTCAACGCCCTCATCGGCTACGACGTGACCGACGTGACG 586
Qy      163 GluSerleuAspGlnuileuArgGlnPhehrarglaSerleuTPalaArgThrlylslys 182
Db      587 AACGTGATGACGATGAGCTG---GAGTTC-----ACGCGGCGC 622
Qy      183 ThrCysleuthrArgglYleuGlnGlyThrSerHisTyralaPheProgluGlnGlnTr 202
Db      623 CGCCTGGTCAC----- 634
Qy      203 LeuysValGlyGluSerCysProlysaPheleuGlnSerlysValylsAlaAlaLysleu 222
Db      635 -----CCCGCATGCGCGAGGTGGCGGCGGCGGACCCCAAGCTT 673
Qy      223 SerTyrglnMetPheTrpArglylsArglys-----AlaGlnIle 235
Db      674 TACGCCATGACACCCCTGGTGATCATCCAAAGCCCTCCCTGATGACTTGTGAAGAATC 733
Qy      236 AsnGlyValCys-----GluYsMetleuLyslleGlnlleGlnuphe 249
Db      734 ACTAAACACTGCGCTTCATGATGATTCACCGGACGACCAACCAACGACATCAAGTGC 793
Qy      250 AsnProaspGlnuThrProlysSerleuLeuHisThrPheleuthrglnuMetArglys 268
Db      794 TCGGCCGATGACACCCGACGAGCACCATCTCCAGAGCTTCTTACCAAGATGCGCAAGAG 853

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QY 269 -----LeuaspValTyrAspThrAspProAlaaspGluGlyTyrPheLeuGln 285
 Db 864 AAATCTCGATGGATATCCCTGAAAGCCAGAAAGGAGAC-----TTTGTCTGGCC 907
 QY 286 LeuAlaGlyArgThrPheValThrAspProAlaaspValTyrPheLeuGln 305
 Db 908 GTCTCGCGCGCGGAGATGAGTACTGGTGGT---GAGAGCCCATCAAAATTTCCAGTGG 964
 QY 306 ValArgSerGluLeuGlnSerTyrArgCysProGlyPheValValArgGlnSerLeu 325
 Db 965 GTGAGCGAGTGCCTCAAGAAAT-----GGGAGAGAGATTAC-----CTT 1003
 QY 326 ValLeuLysAspTyrCysArgProLysProLeuTyrGlnProHisTyrValArgAlaHis 345
 Db 1004 GTTCTGGAC-----ACTCTCAGACCCAGCCCTGGACGAG-----GTGAGAGAGAA 1051
 QY 346 GluArgLysLeuAlaLeuAspValLeuSerValSer-----LAspSerThrProLys 363
 Db 1052 GAGTGGCGCGCTGGTGGATGACGCAAGGAGTCACTGGCTACGAGCAGCTGACATC 1111
 QY 364 GlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSerLeuGln 383
 Db 1112 CACGGCAAGACCATGAAAGTGTGTTCACC----- 1141
 QY 384 ValSerLeuTyrAspLeuAspAlaAsnLeuMetLeuArgProValAsnLeuSerGlyPhe 403
 Db 1142 GTTCTCTGTGGACTGTGACCGCAAGTTCAGGCTCAA-----ATCAGAGGCATT 1192
 QY 404 AspPheProAla-----AspValAspMetTyrValArgLeuGlnPheSerValTyr 420
 Db 1193 GATATCCCTGCTGCTGCGCCGAGACCGCTGACCTCAGCGTGTGTGGAGCAAAATCCAG 1252
 QY 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThr---LysValAsnAlaGlnPheAla 439
 Db 1253 TATGGCAGCAAGTCTTTGGCCAAAGAACCAAGCCCAACCTTCACGAGAGAGTGG 1312
 QY 440 LysTPAsnLysGluMetTyrThrPheAspLeuTyrMetLysAspMetProProSerAla 459
 Db 1313 CTCTGGAACGTGTGCTT---GAGTTCAATTAATAAATCAAAAGCTTACCACCAAGGCGT 1369
 QY 460 ValLeuSerLeuArgValLeuTyrGlyLys-----Val 470
 Db 1370 CTGCTGAACCTCCAGATCTACTGCGGCAAGCTCCAGACGTGTGGCAAGACCTCTGCA 1429
 QY 471 LysLeuLysSerGlnLysPheGlu-----ValGlyTyrValAsnMetSer 485
 Db 1430 GAGATGCCAGTCCCGAGTCCAAAGGCAAGCTCAGCTTCTGTAATGTCAACCTAATGG 1489
 QY 486 LeuThrAspTyrArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeuTyrAlaPro 505
 Db 1490 CTGATAGACACCGCTTCTCTGCGCCATGGCGAGTATGTCTCCACATGTGG----- 1543
 QY 506 GlnProThrAlaAsnArgSerArgLeuGlyLys-----AsnGlyAlaArg 520
 Db 1544 -----CAGTTATCCGGAGAGGGGAAAGCAAGAGGAGCTTCAATGCCGACAG 1591
 QY 521 Ile-----GlyThrAsn-----AlaAlaValThrLeuGlnSer 532
 Db 1592 CTCACGTCGGAAACCAACCCGAGCAAGAGACTCAATGTCCATCTCCATCTTCTGGAC 1651
 QY 533 SerTyrGlyArgValArgMetProSerGlnGlyGlnTyrThrTyrLeuValLysHis 552
 Db 1652 AATTACTGCCACCCCATAGCTTGTCT-----AAGCAT 1684
 QY 553 ArgSerThrTyrThrGlnLeuAsnIleMetGlyAspAspTyrGlnSerCysIleArg 572
 Db 1685 CGG-----CCTACCCCTGACCAAGAGGAGGACCGGAGTGGCAGAAATGCC 1732
 QY 573 AspProGlyTyrTyrLysLeuGlnMetLeuValLysHisGlnSerGlyIleValLeu 592
 Db 1733 AATCAGACTTCGGAAGCACTGAGGAGCAATCATAGCCAGGATCCGTTAAACCATCCACACA 1792
 QY 593 GlnGlnAspGlnGlnArgHisValTyrMetTyrArg---ArgTyrIleGlnLysGlnGln 611

Db 1793 GCTGAAGCAAGAA-----CTGCTCGCATTTCAATATGAAGCTGAAGAT 1843
 QY 612 ProAspLeuLeuIleValLeuSerGluLeuAlaPheValTyrThrAspArgGluAsnPhe 631
 Db 1844 CCCAAAGCGTATCTTAAGCTCTTATGCG---TCGGTGAATGGGAGACCAAGAAATGTG 1900
 QY 632 SerGlnLeuTyrValMetLeuGlnLys-----TyrLysProProSerValAlaAla 648
 Db 1901 GCCAAACATTCCAATTAATTAAGCCAAAGGAGGCTGGGATTCAGAGCTTTGGATGTG 1960
 QY 649 AlaLeuThr-----LeuLeuGlyLysArgCysThrAspArgValIleArgLysPheAla 666
 Db 1961 GGGTTAACCATCAGAGCTCTCTGAGTGCACATCTTCGGATGAAGACGAGAGCCATTGCA 2020
 QY 667 ValGlnLysLeuAsnGlnGlnLeuSerProValThrPheHisLeuPheIleLeuProLeu 686
 Db 2021 GTCCAGAAACTGGAGAGCTTGGAGATGATGACGTGCTCAT---TACCTGCTCCAGCTG 2077
 QY 687 IleGlnAlaLeuLysTyrGlnProArgAlaGlnSerGluValGlyMetMetLeuLeuThr 706
 Db 2078 GTCCAGGCTGTGAATTTGAACCATACCATGACAGTGCCTTACGACATTTCTCTGAAG 2137
 QY 707 ArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTyrLeuLeuArgAlaGlnIle 726
 Db 2138 CGTGGTTTAAGAAACAAGAGATTTGTCACTTTGTTTGTGTTGTTGTAAGAGTGAAT 2197
 QY 727 AlaArgLeuArgAspCysAspLeuLysSerGlnLysTyrArgAlaGlnIleSerLeuLeuMet 746
 Db 2198 GCCCAGCTGTAG-----CACATACAGCAGAGCTTGGCAGTATCTCG 2239
 QY 747 GluAlaTyrLeuArgGly---AsnGlnLysHisLeuIleThrArgGlnValAsp 765
 Db 2240 GAGGCTTACCTGAGAGGCTGTGGCAGACCATGCTGCACAGACTTACCCAGCAAGTCCA 2299
 QY 766 MetValAspGlnLeuThrArgIleSerThrLeuValLysGlyMetProLys----- 782
 Db 2300 GTAATTGACATGTTACAAAGAAAGTCACCATGACATTAATGCTGCTGCGTGAAGATAT 2359
 QY 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsn 802
 Db 2360 GACGTCAGTCTCC-----CAAGTTATTTCCCAACCTTAAGCAAAAGCTTGAAGAAC 2407
 QY 803 MetAspSer-----ProLeuAspProValTyrLysLeu 813
 Db 2408 CTACAGAAATTGATCTCCCAAGCTTTAGAGTCTCTTATGATCTCGAGCTGAAGCC 2467
 QY 814 GlyLysMetIleIleAspLysAlaIleValLeuGlnSerAlaLysArgProLeuMetLeu 833
 Db 2468 GGGGCACTGGATGCAAAATGTAAGTATGAGCTCTCAAGAAAGAGCCCTGTGGCTT 2527
 QY 834 HisTyrLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIlePhe 853
 Db 2528 GAGTTTAATATGCGCATCTTACCGCT---CTATCAATGAAGAACAAATTTGAATTTCTT 2584
 QY 854 LysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValIleMetAsp 873
 Db 2585 AATCAGGTGACATCTCGCCCAACACATGCTTATTTACGATTTCAATCATATGAGAG 2644
 QY 874 AsnIleTyrLysAlaAlaAsnIleAspCysCysLeuAsnProTyrAlaValLeuProMet 893
 Db 2645 TCCATTTGGAGACCGAATCTTTGGATCTGTGCTCCGCAATATGCTGCATTTCAACT 2704
 QY 894 GlyLysMetIleGlyIleIleGlnValValProAsnLysLysThrIlePheGlnIleGln 913
 Db 2705 GGTGAACAATTAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2764
 QY 914 ValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPheMetAsnLys 933
 Db 2765 CAAGACACA---GTGGCAACACGGGT---GCCTTAAGATGAAGTCTTGAAGTCAAC 2815
 QY 934 TyrIleArgLysGlnCysGlyIleGlnAspGlnLysLysSerLysLysAspSerThr 953

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Db      2816 TGGCTCAAGAAAAATGCCCTATTGAGAA----- 2845
Qy      954 LysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyrPheGluSer 973
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Qy      974 ValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIleMetGlyLe 993
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Qy      994 LysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrValHisIleAsp 1013
Db      2921 GCGGACAGACACAAATGACAAATTTATGATCAGAAACGAAATCTATTATTTGAT 2980
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Qy      1034 PheIleLeuThrGluHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsn 1053
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Qy      1054 SerHisGluLeuGluLysPheLysThrLeuGlyValGlnAlaTyrGluValMetTyrAsn 1073
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Qy      1114 GluGluAlaArgLysPhePheAlaGlyLeuTyrGluGluAlaPheAsnGlySerTyrSer 1133
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RESULT 14
US-08-972-630-3
; Sequence 3, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.

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/      REGISTRATION NUMBER: 25,277
/      REFERENCE/DOCKET NUMBER: 8549-0005-999
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (415)854-3660
/      TELEFAX: (415)854-3694
/      INFORMATION FOR SEQ ID NO: 3:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 3808 base pairs
/      TYPE: nucleic acid
/      STRANDEDNESS: single
/      TOPOLOGY: unknown
/      MOLECULE TYPE: cDNA
/      US-08-972-630-3

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Score:          1038.00      Matches:      316
Percent Similarity: 46.96%      Conservative: 224
Best Local Similarity: 27.48%      Mismatches: 400
Query Match:    17.17%      Indels:      210
DB:             2      Gaps:      46

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Qy      83 LeuIleAlaProMetLysTyrGlyThrTyrSerValLysProGlnAspTyrValPheArg 102
Db      380 CTGGCTTCCAGAAAGAGGAGGAGGTGACAGATCTATGACAAAGTACAGATGAGTGCAG 439
Qy      103 GlnLeuAsnAsnPheGlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLys 122
Db      440 ACCCTGACCTCCGCTGCTACTGAGAGGTGTGACACCGACCCCGGCGAGATCCAGCTG 499
Qy      123 LeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArg 142
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Qy      143 AspLysGluLeuMetSerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGlu 162
Db      542 -----CGCCAGCTCAACGCCCTCTACGCTACGACGTCAACGACGTCAACG 586
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Qy      183 ThrCysLeuThrArgGlyLeuGluGlyThrSerHisTyrAlaPheProGluGluGlnTyr 202
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Db      635 -----CCGGCATGCGCGAGGTGGCGGCGCGGACCCCAAGCTT 673
Qy      223 SerTyrGlnMetPheTyrPargLysArgLys-----AlaGluIle 235
Db      674 TACGCCATGACACCCCTGGGTGATCCAAAGCCCTCCCTGAGTACCTTCTGAAAGATC 733
Qy      236 AsnGlyValCys-----GluLysMetMetLysIleGlnIleGluPhe 249
Db      734 ACTAACAACCTGCGCTTCATGCTATTCACCGGACACACACAGCCAGACCATCAAGTTC 793
Qy      250 AsnProAsnGluThrProLysSerLeuLeuHisIleThrPheLeuTyrGluMetArgLys--- 268
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Oy	404	AspPheProIa-----AspValAspMetTyArgIleGluPheSerValTyR	420
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Oy	421	ValGlyThrLeuThrLeuAlaSerLysSerThrThr-----LysValAsnAlaGlnPheAla	439
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Oy	440	LysThrPheLysGluMetTyThrPheAspLeuTyMetLysAspMetProProSerAla	459
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Oy	460	ValLeuSerIleArgValLeuTyGlyLys-----ValIleTyPValAsnMetSer	470
Db	1370	CTGTGTAACTCTCCAGATATTACTGGGGCAAAAGTCCACACGTGTGGCAAGACTCTGCA	1429
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Db	1490	CTGATAGCAACCGCTTCTCTCTCCGCGCATGGCAGATGTGCTCACATGTGG-----	1543
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Db	1544	-----CAATTATCCGGGAAGGGGAAACCAAGGAGCTTCATCCGCAAG	1591
Oy	521	Ile-----GlyThrAsn-----AlaAlaValThrIleGluIleSer	532
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Db	1685	CGG-----CTTACCCTGACCCCAAGAGGAGCGGGTTCCGGGCAAGAAATGCC	1732
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Oy	632	SerGluLeuTyTyValMetLeuGluLys-----TrpLysProProSerValAlaAla	648
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Qy	707	ArgAlaLeuCyAspIYrArgIleGlyHisArgLeuPheTrpLeuLeuArgAlaGlyIle	726
Db	2138	CGTGGTTTAAAGAAACAGAGAAATGGTGCACCTCTCTTTGGTCTCTTGAGAAAGAGACATT	2197
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Qy	747	GluAlaIYrLeuAsnGly--AsnGlnGlnHisIleIYrIleTrpArgGlnValAsp	765
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Qy	766	MetValAspGluLeuTrpArgIleSerThrLeuValIYrGlyMetProLys-----	782
Db	2300	GTAATTGACATTTCACAAAGATCAACCATCACTTAATAGCTCTCTGCTGGAAGAAGAT	2359
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Db	2360	GACGTCAGTCC-----CAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAC	2407
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Job time : 315 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2003, 05:04:05 ; Search time 852 Seconds
(without alignments)
1882.476 Million cell updates/sec

Title: US-08-908-453-1

Perfect score: 6046

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Searched: 870385 segs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62
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Database :

Published Applications_NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6046	100.0	3504	10	US-09-205-658-47	Sequence 47, Appl
2	6046	100.0	3504	10	US-09-844-353A-47	Sequence 47, Appl
3	1033	17.1	5220	9	US-10-027-591-1	Sequence 1, Appl
4	1031	17.1	3387	9	US-10-162-160-2	Sequence 2, Appl

5	668	11.0	5990	10	US-09-917-800A-477	Sequence 477, App
6	624	10.3	5061	12	US-10-092-219-1	Sequence 1, Appl
7	551.5	9.1	3252	10	US-09-921-332-1	Sequence 1, Appl
8	551.5	9.1	3252	10	US-09-921-330-1	Sequence 1, Appl
9	551.5	9.1	3252	10	US-09-921-329-1	Sequence 1, Appl
10	399	6.6	2418	10	US-09-771-161A-10	Sequence 10, Appl
11	325	5.4	5703	10	US-09-801-368-389	Sequence 389, App
12	309	5.1	2620	10	US-09-925-102-205	Sequence 205, App
13	278	4.6	7864	10	US-09-834-975-805	Sequence 805, App
14	257.5	4.3	2451	10	US-09-976-165-25	Sequence 25, App
15	257.5	4.3	2487	10	US-09-976-165-32	Sequence 32, App
16	257.5	4.3	3324	10	US-09-976-165-33	Sequence 33, App
17	257.5	4.3	3602	10	US-09-976-165-30	Sequence 30, App
18	228	3.8	339	9	US-09-796-692-7359	Sequence 7359, App
19	228	3.8	339	9	US-10-040-862-7359	Sequence 7359, App
20	218.5	3.6	9385	9	US-10-175-225-1	Sequence 1, Appl
21	215.5	3.6	9171	10	US-09-810-993-1	Sequence 1, Appl
22	215.5	3.6	9196	8	US-08-984-090-1	Sequence 1, Appl
23	215	3.6	326	9	US-09-796-692-7451	Sequence 7451, App
24	215	3.6	326	9	US-10-040-862-7451	Sequence 7451, App
25	191.5	3.2	3423	9	US-09-950-634-2	Sequence 2, Appl
26	191.5	3.2	7653	9	US-09-950-634-1	Sequence 1, Appl
27	191.5	3.2	8741	9	US-10-198-846-11285	Sequence 11285, App
28	186.5	3.1	441	10	US-09-867-701-5505	Sequence 5505, App
29	179.5	3.0	8838	9	US-09-957-837A-1	Sequence 1, Appl
30	178.5	3.0	4074	10	US-09-764-877-3796	Sequence 3796, App
31	169	2.8	8210	10	US-09-962-436-279	Sequence 279, App
32	158.5	2.6	1894	10	US-09-771-161A-11	Sequence 11, Appl
33	154.5	2.6	4610	9	US-09-957-837A-4	Sequence 4, Appl
34	154.5	2.6	4651	9	US-09-957-837A-3	Sequence 3, Appl
35	154.5	2.6	4651	9	US-09-957-837A-5	Sequence 5, Appl
36	141	2.3	2970	9	US-10-270-333-133	Sequence 133, App
37	139	2.3	3640	9	US-09-292-758-144	Sequence 144, App
38	137	2.3	466	9	US-09-918-995-35578	Sequence 35578, App
39	136	2.2	3859	9	US-10-097-340-3	Sequence 3, Appl
40	136	2.2	3859	10	US-10-163-587A-3	Sequence 3, Appl
41	136	2.2	3859	10	US-09-864-664-300	Sequence 300, App
42	130.5	2.2	4424	9	US-10-245-175-1	Sequence 1, Appl
43	129.5	2.1	3720	9	US-10-076-632-576	Sequence 576, App
44	129.5	2.1	3720	12	US-10-007-805-576	Sequence 576, App
45	128	2.1	436	9	US-09-918-995-857	Sequence 857, App

ALIGNMENTS

RESULT 1
US-09-205-658-47
; Sequence 47, Application US/09205658
; Patent No. US20010029617A1
GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-47
Alignment Scores: 0
Pred. No.: 0
Length: 3504

Score:	6046.00	Matches:	1146
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-08-908-453-1 (1-1146) X US-09-205-658-47 (1-3504)

OY	1	MethSVLAAnIleLeuNIaProGluLeuGlnThMetValGluIleIrrProGlnMetAG	20
Db	64	ATGCATGTTAAACATTTTACATCCACAACTGCAAACGATGGTCAGACAGTGGCAATGCCA	123
OY	21	GluaTgProSeLeuGluThGluAnGlyLyGlySeLeuLeuLeuGluAnGlyLy	40
Db	124	GAAGCCCATCGCTGGAGACCGAGAAATGGCAAAAGATCCGCTGCTCGGAATAATGAAGGT	183
OY	41	ValAlaAerIleIleThMetCybProPheGlyGluValIleSerValValPheProTrp	60
Db	184	GTCCGAGATATCATCACTATGTGTCCATTCGGAGAAATTAAAGTATGATATTTCCGTGG	243
OY	61	PheLeuAlaAerValArgThrSerLeuGluIleLeuLeuSerAerPheLeuSHIsgIleu	80
Db	244	TTTCTTCGAATGTGGCGAACATCGCTGAATACMACTATCCAGATTCCAAATCAACT	303
OY	81	PheGluLeuIleAlaProMetLeuStrpGlyThrTySerValIleProGlnAerTyVal	100
Db	304	TTCCGAATGATGTCTCCGATGAAGTGGGGAACATATTCGTTAAAGCCACAGATATGTGTG	363
OY	101	PheAaGluIleLeuAerAerPheGlyGluIleGluValIlePheAerAerArgGlnProLeu	120
Db	364	TTCCACACAGTTGAATTAATTTGGCGAAATTTGAAGTTATTTTAAACACAGATCAACCCCTG	423
OY	121	SerTyLeuGluLeuNIaIsgIlyThrPheProMetLeuPheLeuTyGlnProAerGlyIle	140
Db	424	TCGAATTTAGACCTCCACGCACTTTCCCAACGCTTTTCTGACCAACTGATGGAAAT	483
OY	141	AerAaGArLeuGlyLeuNIaMetSerAerIleSerNIaCyaleuGlyTyTySerLeuAerLy	160
Db	484	AACAGCGATTAAGAATTAATGATGATATATAGCATGTCCTGAGGATACACAGTGAATAA	543
OY	161	LeuGluGluSerLeuAerGluGluLeuAaGluGlnPheAaGlyAerLeuTrpAlaAaGlyTr	180
Db	544	CTGGAAAGAGGCTCGATAGGAACCTCCGTCATTTGCGCTCTCTCTGCGGCTCGTACG	603
OY	181	LyAlaTyThrCyaleuThzArgGlyLeuGluGlyTyThrSerNIaTyzAlaPheProGluGlu	200
Db	604	AAGAAACAGCTGTTGACAGCTGGACTTGAAGGATACAGATCAAGCGTTCCCGCAAGAA	663
OY	201	GlnTyGLeuCyaleuAlaGlyLeuSerCybProLyAerPheGluLeuTyValIleValAla	220
Db	664	CAGTACTGTGTGTGGTGAATCGTCCCGAAAGATTTGGAAATCAAAAGCTCAAGGCTGCC	723
OY	221	LyLeuAerSerTyGluMerPheTrpArgLyAaGlyValAAGluIleAnGlyValCyaleu	240
Db	724	AAGCTGAGTTATACAGATGTTTGGACAAAACGAAAGCGGAATCAATGAGATTGGAG	783
OY	241	LyMetMetLeuAlaIsgIleGluPheAerProAerGluTyThrProLySerSeLeuLeuNIa	260
Db	784	AAATATGATGAAGTTCAATTTGAATTCATTCGAAACGAACATCCGAATCTCGCTTCC	843
OY	261	ThrPheLeuTyGlyMeAaGlyLeuAerValTyzAerThrAerAerProAlaAerGly	280
Db	844	ACGTTTCTCTACGAATTCGAAATTTGATGTATACGATACCAATATCTCTGACATGAA	903
OY	281	GlyTrpPheLeuGluLeuAlaGlyAaGlyTrpThrPheValThzAerProAerValIleLeu	300
Db	904	GGATGGTTTCTTCAATTTGGCTGGACGTTACACGTTGTTACAAATGCAAGTCCAACTT	963
OY	301	ThzSerTyzAerGlyValAaGserGlyLeuGluLeuTyzAerGlyCybProGlyPheVal	320
Db	964	ACGCTTTATGATGCTGCTCGTTGCGAACTGGAAGGATATGATGAGCTCGGATTCGTTGTT	1022
OY	321	ArgAaGlnSerLeuValLeuLyAerTyTyzAerProLyAerLeuTyGluIrrProNIa	340

Db	1204	CGCCGACAAATCACTAGTCTCAAAGACATATTGTGCGCCAAAACCACTGTACGAACCAAT	1083
QY	341	TYrVALArGALaHrGLuArGLyLeuVALLeuAspVALLeuSerVALSerILLeaSPSer	360
Db	1084	TATGTGAGAGACACAGAAACCACTTGCTCTACACGCTCAGCGTGTCTATGATGTGC	1143
QY	361	ThrProLYSGInSerLYrAsnSerASPmetVALmetThrASPmetARGProthRALSer	380
Db	1144	ACACCAAAACGACCAAGAACAGACAGTGTATGACTGATTTTCGTCGCACAGCTTCA	1203
QY	381	LeuLYSGInVALSerLeuTRPASPLeuAspVALAsnLeuMetILEARProVALAsnILE	400
Db	1204	CTCAACAAAGTTTCACTTTGGGACCTTGACCGCAATCTTATGATACGGCTGTGAATATT	1263
QY	401	SerGLYPheaSPheProVALAspVALAspMetTYrVALArgILEuPheSERVALTYr	420
Db	1264	TCTGGATTTCGATTTCCGGCCGACGTGGATATGTATACGTTCCAAATTCGAATTCAGTGTATAT	1322
QY	421	VALGLYThrLeuThrLeuVALSerLYSerThrThrLYSVALAsnALeGInPheALaYS	440
Db	1324	GTTGGGACACACGACGCTGGCATCAAAATCTACACAAAGAGAAATGCTCAATTGGCAAA	1383
QY	441	TRPAsnLYSGInMetTYrThrPheASPLeuTYrMetLYSASPmetProProSERVALVAL	460
Db	1384	TGGATATAGGAATATGTACACTTTTGATCTTATACATGAAGATATGCCACCATCTGCATTA	1443
QY	461	LeuSERILEARGLValLeuTYrGLYLYVALLYSLeuLYSserGLInuPheGLUVALGLY	480
Db	1444	CTCAGCATTTCCGTGTTTGTACGGAAGATGTAAATTAAAGATGAAGATTCCGAAGTTGGT	1503
QY	481	TRPVALAsnMetSerLeuThrASPTRPARGAspGLULeuARGInGLInPheLeuPhe	500
Db	1504	TGGGTAATATATGTCCCTACCGATTTGAGAAATGAATCAACAGCAAGCAAAATTTTATTC	1563
QY	501	HisLeuTRPALProGLUProThrALAsnARGSerArgILEGLYAsnGLYALAARG	520
Db	1564	CATCTGTGGGCTCTGGAACCACTGCCATGTGTAGTACGATCGAGAGAAAATCGAGCAAG	1622
QY	521	ILEGLYThrAsnVALValValThrILEGLInuLeuSERTYrGLYLYARGVALARGMet	540
Db	1624	ATAGGACCAACGACGCGGTATACAAATTGAATCTCAATGTATGGGTAGAGTTGCAATG	1683
QY	541	ProSerGLInGLYInTYrThrTYrLeuVALLYSHASARGSerThrTRPThrGLInuThrLeu	560
Db	1684	CCGAGTCAAGACCAATACATACATCTCTGCACGACCCGAAGTACTTGACCGAAACTTGTG	1743
QY	561	AsnILEMetGLYASPASPtyrGLYserCYSLLeARGAspProGLYTYrLYSLeuGLIn	580
Db	1744	AATATATTAGGGTATGACTATGATGATCGTGTATCAGAGATCCAGAGATATACAGAACTTCAG	1803
QY	581	MetLeuVALLYSLYSHLeuSERGLYILEVALLeuGLInuASPGLInuARGInVAL	600
Db	1804	ATGCTGTTCGAAGAGCATGAATCTCGAATTGTATTAAGAGAAAGAACCAACGTCATGTC	1863
QY	601	TRPMetTRPARGARGTYrILEGLInuLYSGLInuProASPLeuLeuILEVALLeuSERGLIn	620
Db	1864	TGGATGTGAGAGAGATACATTCAAAAGACAGAGCGCTGATTTGCTCATTTGTCTCTCCAA	1923
QY	621	LeuVALPheVALTRPThrASPARGInuAsnPheSERGLULeuTYrVALMetLeuGLInuYS	640
Db	1924	CTCGCATTTGTGTGACTGATCGTGAACCTTTTCGAGCTCTATGTATGCTTGAAAAA	1983
QY	641	TRPLYSProProSERVALALAsnALeUTHrLeuLeuGLYLYSARGCYSThrASPARG	660
Db	1984	TGGAAACCGCCGAGGTGTGGACGCCGCTTGACTTTGGAAAAAGTTGACCGGATCGT	2043
QY	661	VALILEARGLYSPheALVALGLInuLYSLeuGLInuLeuSERProVALThrPheHIS	680
Db	2044	GTCATTCGAAAGTTTGACGTGAGAGAAATGTGAATGACGCTGAGCCGCTCATTTCCAT	2103
QY	681	LeuPheILEuProLeuILEGLInuALeuLYSTYrGLInuProARGALeGLSerGLUVAL	700

Db 2104 CTTTCATATGCTCTCATACAGCGCTTGAGATGACGACCGCTCAATCGAGATT 2163
 Qy GlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTyr 720
 Db 2164 GGAAATGAGCTCTTACTAGAGCTCTCTGCGATATTCGATATGCAATGAGATCGATCTTTCGG 2223
 Qy LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLeuSerGlyLeuTyrArg 740
 Db 2224 CTGCTCCGTGACGAGATTGCTGTTGAGAGATTGTGATCTGAAAAAGGAGAAATATCGC 2283
 Qy ArgIleSerLeuLeuMetGluAlaTyrLeuArgGlyAsnGluHisIleLeuIle 760
 Db 2284 CGATCTCACTCTCGATGAGAGCTTACCTCCGTGAAATGAGACACATCAATGATTCATC 2343
 Qy ThrArgGluValAspMetValAspGluLeuThrArgIleSerThrLeuValIleGlyMet 780
 Db 2344 ACCGACAAAGTTGACATGTTGATGATGCTCACACAAATCGACATCTTGTCAAAGGAATG 2403
 Qy ProLysAspValAlaThrMetLeuLeuArgAspGluLeuArgSerIleSerHisLysMet 800
 Db 2404 CCAAAAGATGTTGCTACGATGAACTGGCGTACGAGCTTCGATCGATTAGTATTAATG 2463
 Qy GluLeuMetAspSerProLeuAspProValTyrTyrLeuGlyGluMetIleLeuAspLys 820
 Db 2464 GAAATATGATTCCTCCACTGATCTGTGTACAACTGGGTGAATGATATATTCACAA 2523
 Qy AlaIleValIleGluSerAlaLysArgProLeuMetLeuHisIleTyrLysAsnLysAsnPro 840
 Db 2524 GCCATCGTCTTACGAAAGTGCACAAAGCTGTTAATGCTTCACTGGAAGAACAAATTCAC 2583
 Qy LysSerAspLeuHisLeuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuArg 860
 Db 2584 AAGAGTGACCTGCACCTTCGTTCTGTGCAATGATCTTCAGAAATGAGAGCATCTTCCG 2643
 Qy GluAspMetLeuValLeuGluValLeuGluValMetAspAsnIleTyrLysAlaAlaAsn 880
 Db 2644 CAGGACATGCTGTTCTTCAAGTTCTCGAAGTTATGATGATTCGAAAGCTGTCACAA 2703
 Qy IleAspCysValLeuAsnProTyrAlaValLeuProMetGlyGluMetIleGlyIleIle 900
 Db 2704 ATTGATCTGTTTAAACCCGATCCGATCTTCGAAAGGAGAAATGATGAAATATAT 2763
 Qy GluValValProAsnCysLeuThrIlePheGluIleGluValGlyThrGlyPheMetAsn 920
 Db 2764 GAAGTGGCCATATGTTAAACATATTCGAGATTCGAAGTTGGAACGATTCATGAT 2823
 Qy ThrAlaValArgSerIleAspProSerPheMetAsnLysTyrIleArgLysGluCysGly 940
 Db 2824 ACAGCAGTTCGAGATGATTCCTTCGTTATGAAATGATGATTCGAAACAAATGCGGA 2883
 Qy IleGluAspGluValLeuSerLysSerLysAspSerThrLysAsnProIleGluLysLys 960
 Db 2884 ATTGAAGATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2943
 Qy IleAspAsnThrGluAlaMetLeuLysLysTyrPheGluSerValAspArgPheLeuTyrSer 980
 Db 2944 ATTGATATATCTCAAGCATGAAAGAAATATTTGAAAGTGCATCGATTCCTATACCG 3003
 Qy CysValGlyTyrSerValAlaThrTyrIleMetGlyIleLysAspArgHisSerAspAsn 1000
 Db 3004 TGTGTTGATATATTCAGTGGCCACGATCAATATGGAATCAAGATCGTCACAGTATAT 3063
 Qy LeuMetLeuThrGluAspGlyLysTyrValHisIleAspPheGlyHisIleLeuGlyHis 1020
 Db 3064 CTGATCTCACTGAAGATGAAATATGTCACATGATGATTCGGTCACATTTTGGGACAC 3123
 Qy GlyLysThrLysLeuGlyIleGluArgAspArgGlnProPheIleLeuThrGluHisPhe 1040
 Db 3124 GGAAGACCAAACTGGGATCCAGCGAGATGTCACACGTTATATCTAAACGAAACACTT 3183
 Qy MetThrValIleArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGluLysPhe 1060
 Db 3184 ATGACAGATTCATCGGATTAATCTGTGATGAAATTCGATGAGCTACAAAATTC 3243

Qy 1061 LysThrLeuCysValGluAlaTyrGluValMetTyrAsnAsnArgAspLeuPheValSer 1080
 Db 3244 AAAAGCTTATCGTCGAAAGCTTACGAAATGATGGAATATTCGAAATTTGTTGCTTCC 3303
 Qy LeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrTyrValAspLeuAsp 1100
 Db 3304 TTGTTACCTTGAATGCTCGAATGAGATGAGTTCCTGAGCTGTGACGAAACCGGATTTGGAT 3363
 Qy HisLeuLysLysThrLeuPheCysAsnGlyLysLysTyrGluGluAlaArgLysPhePhe 1120
 Db 3364 CATTGAGAAAGAACCTCTTTCGAAATGAGAAAGAAAGAAAGAAAGAAAGAAAGTTTTC 3423
 Qy AlaGlyIleTyrGluGluAlaPheAsnGlySerTyrPheSerThrLysAsnTyrLeuPhe 1140
 Db 3424 GCTGGAATCTCGAAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 3483
 Qy 1141 HisAlaValLysHisTyr 1146
 Db 3484 CACGAGTCAAACACTAC 3501

RESULT 2
 US-09-844-353A-47
 ; Sequence 47, Application US/09844353A
 ; Patent No. US20020037585A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruvkun, Gary
 ; APPLICANT: Kimura, Koutarou
 ; APPLICANT: Patterson, Garth
 ; APPLICANT: Ogg, Scott
 ; APPLICANT: Paradisi, Suzanne
 ; APPLICANT: Tissenbaum, Heidi
 ; APPLICANT: Morris, Jason
 ; APPLICANT: Kowsek, Allison
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
 ; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 ; FILE REFERENCE: 00786/351005
 ; CURRENT APPLICATION NUMBER: US/09/844,353A
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 08/857,076
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 3504
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 US-09-844-353A-47

Alignment Scores:
 Pred. No.: 0 Length: 3504
 Score: 6046.00 Matches: 1146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-08-908-453-1 (1-1146) x US-09-844-353A-47 (1-3504)
 Qy 1 MethiValAsnIleLeuHisArgGluLeuGluThrMetValGluGluIntTyrGluMetArg 20
 Db 64 ATGATGTTTAACTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 123
 Qy 21 GluArgProSerLeuGluThrGluAsnGlyLysGlySerLeuLeuGluAsnGluGly 40
 Db 124 GAAAGCCCATGCTGGAAGACCGAAGATGCGAAGATGCGCTCCGGAAGAAATGAAAGCT 183
 Qy 41 ValAlaAspIleIleThrMetCysProPheGlyGluValIleSerValAlaPheProTyr 60
 Db 184 GTCCGAGATATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
 Qy 61 PheLeuAlaAsnValArgThrSerLeuGluIleLysLeuSerAspPheLysIleGluLeu 80

Db 244 TTTCTGCAATGTGCGAATCATGCTAGAAATCAAGTATTCAGATTTCAGAAATGCACTT 303
Qy 81 PheGluLeuIleAlaProMetLysTrpGlyThrTyrsSerValLysProGlnAspTyrVal 100
Db 304 TTCGAATTGATTGCTCCGATGAGATGGGGAACATATTCGTTAAACCCACAGATTATGTG 363
Qy 101 PheArgGlnLeuAsnAspPheGlyGlnIleGluValIlePheAsnAspAspGlnProLeu 120
Db 364 TTCAGACAGTTGAATTAATTCGCGAATTAAGTTATTAATTAACAGCATCAACCCCTG 423
Qy 121 SerLysLeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyLe 140
Db 424 TCGAATTAAGACTCCACGGCACTTTCCCAATGCTTTTCTTACCAACTGATGGAATA 483
Qy 141 AsnArgAspLysGluLeuMetSerAspLysSerHisGlyLeuGlyTyrSerLeuAspLys 160
Db 484 AACAGGATTAAGAAATTAATGATGATTAATAGTCAATTCCTAGGATACCTGATGAATA 543
Qy 161 LeuGluGlnSerLeuAspGlnGluLeuArgGlnPheArgAlaSerLeuTrpAlaArgThr 180
Db 544 CTGGAAGAGAGCTCGATGAGAACTCCGTCAAATTCGTCTCTCTGGGCTGTAG 603
Qy 181 LysLysThrCysLeuThrArgLysLeuGlnGlyThrSerHisTyrAlaPheProGlnGlu 200
Db 604 AAGAAACGCTGCTTGACAGTGGACTTGAGGGTACCACTACCTACGCGTCCCGAAGA 663
Qy 201 GlnTyrLeuCysValGlyGlnSerCysProLysAspLeuGlnSerLysValIleAla 220
Db 664 CAGTCTGTGTGTGGTGAATCGTGCCGAAAGATTGGAAATCAAAATGCAAGGTGCG 723
Qy 221 LysLeuSerTyrGluMetPheTrpArgLysArgLysAlaGluIleAsnGlyValCysGlu 240
Db 724 AAGCTGAGTTACAGATGTTTGGAGAAACCTTAAGCCGAATCAATGAGATTGCGAG 783
Qy 241 LysMetMetLysIleGlnIleGluPheAsnProAsnGlnThrProLysSerLeuLeuHis 260
Db 784 AAAATGATGAAATTCAAATTTGAAATTCATCCGAAGAACTCCGAAATCTCGTCTCAC 843
Qy 261 ThrPheLeuTyrGluMetCysLysLeuAspValTyrAspThrAspAspProAlaAspGlu 280
Db 844 AGCTTCTTACGAAATGCGAAATTTGATGATAGATACGATCCGATATCTCCAGATGA 903
Qy 281 GlyTrpPheLeuGlnLeuAlaGlyArgThrThrPheValThrAsnProAspValLysLeu 300
Db 904 GGAATGTTCTTCAATGCTGAGCTGAGCTACCACTGTTGTTCAATCAATGATCAACTT 963
Qy 301 ThrSerTyrAspGlyValArgSerGlnLeuGlnSerTyrArgCysProGlyPheValVal 320
Db 964 ACGTCTTATGATGTGTCCGTTCCGAACTGGAAGCTATCGATGCCCTGGATTGCTGTT 1023
Qy 321 ArgArgGlnSerLeuValLeuLysAspTyrCysArgProLysProLeuTyrGluProHis 340
Db 1024 CCGCGCAATCACTAATCTCTCAAGACTATGTGCGCCAAACCACTTACGAAACCACT 1083
Qy 341 TyrValArgAlaHisGlyLysArgLysLeuAlaLeuAspValLeuSerValSerIleAspSer 360
Db 1084 TATGTAGAGCACACGAAACGAAACTTCTCTAGACGTGCTCAGCGTCTCTATAGTATAC 1143
Qy 361 ThrProLysGlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSer 380
Db 1144 ACACCAAAACAGAGCAAGAAACAGTGCATGTGTTATGATGATTTGCTCGACAGCTTCA 1203
Qy 381 LeuLysGlnValSerLeuTrpAspLeuAspAlaAsnLeuMetIleArgProValAsnIle 400
Db 1204 CTCAAACAAAGTTCACTTGGGACCTTGACGCGAACTTAATGATAGGCGCTGGAAATTT 1263
Qy 401 SerGlyPheAspPheProAlaAspValAspMetTyrValArgIleGluPheSerValTyr 420
Db 1264 TCTGATTTGATTTCCCGCGCCAGCTGATATGTACGTTGCAATTCAGATGATATAT 1323
Qy 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThrLysValAsnAlaGlnPheAlaLys 440
Db 1324 GTGGGACACTGACGCTGGCATCAAAATCTACAAACAAAGTGAATGCTCAATTTGCAAAA 1383

Qy 441 TrpAsnLysGluMetTyrThrPheAspLeuTyrMetLysAspMetProProSerAlaVal 460
Db 1384 TGGATTAAGAAAGTAACTATTGATCTATACATGAAGATATAGCCACATCTGCAGTA 1443
Qy 461 LeuSerIleArgValLeuTyrGlyLysValLysLeuLysSerGlnGluPheGluValGly 480
Db 1444 CTCAGCATTCGTGTTTCTACGAAAGTGAATTAAGATGAAGATTCGAAGTTGCT 1503
Qy 481 TrpValAsnMetSerLeuThrAspTrpArgAspGluLeuArgGlnGlyGlnPheLeuPhe 500
Db 1504 TGGGTAATATGTGCTTAAACCGATGAGATACACTACACAGCAAGCAATTTTATTC 1563
Qy 501 HisLeuTrpAlaProGlnProThrAlaAsnArgSerArgIleGlyLysAsnGlyAlaArg 520
Db 1564 CATCTGTGGCTCTCGAACCACTGCAATCTGTAGTACGATCGAGAAATGAGAGCAAG 1623
Qy 521 IleGlyThrAsnAlaAlaValThrIleGluLysSerSerTyrGlyArgValArgMet 540
Db 1624 ATAGGCACCAACGACGCGTTACAAATTAATCTCAAGTTATGCTGTAGATTGCAATG 1683
Qy 541 ProSerGlnGlyGlnTyrThrTyrLeuValLysHisArgSerThrTrpThrGluThrLeu 560
Db 1684 CCGAGTCAAGACAAATACATATCTCGTCAAGACCCGAACTACTTGGACGGAACCTTGG 1743
Qy 561 AsnIleMetGlyAspAspTyrGlnSerCysIleArgAspProGlyTyrLysLysLeuGln 580
Db 1744 AATATTAATGAGGTGATGATTAAGTCGTGATACAGATACCAAGATATTAAGAGCTTCAG 1803
Qy 581 MetLeuValLysLysHisGluSerGlyIleValLeuGlnGluAspGlnArgHisVal 600
Db 1804 ATGCTTGTCAGAAAGCATGAAATCGAATTTGATTAAGAAATGAACCAACGTCATGTC 1863
Qy 601 TrpMetTrpArgArgTyrIleGlnLysGlnGluProAspLeuIleValLeuSerGlu 620
Db 1864 TCGAGTGTGAGAGATACATCAAAAGCAGAGCTGATTTGCTCATTTGTCTCCCAA 1923
Qy 621 LeuAlaPheValTrpThrAspArgGluAsnPheSerGluLeuTyrValMetLeuGluLys 640
Db 1924 CTGCAATTTGTGTGACTGATCTGAGAACTTTCCAGCTCTATGTGATGCTTGAAATA 1983
Qy 641 TrpLysProProSerValAlaAlaAlaLeuThrLeuLeuGlyLysArgCysThrAspArg 660
Db 1984 TGGAAACCGCGAGGTGTGGACCGCGCTTGACTTGTGTAAGAAACGTTGACCGATCGT 2043
Qy 661 ValIleArgLysPheAlaValGluLysLeuAsnGlnLeuSerProValThrPheHis 680
Db 2044 GTGATTCGAAAGTTTGGAGTGAAGATGATGAGCAGCTGAGCCGCTCACATTTCCAT 2103
Qy 681 LeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGluProArgAlaGlnSerGluVal 700
Db 2104 CTTTTCATATTTGCTCTTATACAGGCTTGTAAGTGAACCGCGCTCAATCGGAATT 2163
Qy 701 GlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTrp 720
Db 2164 GGAATGAGCTCTTACATAGCTCTGCGCAATTAATGAAATGACATCGACTTTCTGG 2223
Qy 721 LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGlnGluTyrArg 740
Db 2224 CTGCTCCGTGACGAAATGCTGCTTGTGAGAAATGTGATCGAAAGAAAGAAATATGC 2283
Qy 741 ArgIleSerLeuLeuMetGluAlaTyrLeuArgGlyAsnGlnGluHisGlyLysIleLe 760
Db 2284 GGTATCTCACTTCTATGAGAGCTTAATCTCCGTGAAATGAAGACATCAAGATCATC 2343
Qy 761 ThrArgGlnValAspMetValAspGluLeuThrArgIleSerThrLeuValLysGlyMet 780
Db 2344 ACCGACAAAGTTGACATGTTGATGAGCTCACAGAAATCAGACACTTGTCAAGGAATG 2403
Qy 781 ProLysAspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMet 800
Db 2404 CCAAAAGATGTTGTACATGAAGAACTGGGTGACGAGCTTGATTCATTAATTAATG 2463

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QY 801 GluAsnMetAspSerProLeuAspProValTyrTyrLeuGlyGluMetIleIleAspLys 820
Db 2464 GAAATATATGATTTCCACTGATCTCTGTATCAAACTGGTGAATATATCGACAA 2523
QY 821 AlaIleValLeuGlySerAlaLysArgProLeuMetLeuHisTyrLysAsnLysAsnPro 840
Db 2524 GCCATCGCTCTAGGAAGTGCMAAACGTCGTAAAGCTTCACTGGAAGAAACAAATCCA 2583
QY 841 LysSerAspLeuHisIleuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuArg 860
Db 2584 AAGATGACCTGACCTTCCCTTCTGTGCAATGATCTTCAAGAAAGGAGACATCTTCGC 2643
QY 861 GluAspMetLeuValLeuGlnValLeuGlnValMetAspAsnIleTyrLysAlaIleAsn 880
Db 2644 CAGGACATGCTTCTTCAAGTTCCTGAAAGTTAAGATTAATCATCGAAGGCTGCAGAAC 2703
QY 881 IleAspCysCysLeuAsnProTyrAlaValLeuProMetGlyGluMetIleGlyIleIle 900
Db 2704 ATTGATTCGTGTTTAAACCCGTACGACAGTTCCTCAATGGGAGAAATGATTGAAATTAT 2763
QY 901 GluValValProAsnCysLysThrIlePheGlnIleGlnValGlyTyrGlyPheMetAsn 920
Db 2764 GAAATGTCCTTAATGTAAACAAATATCGAATTCAGATTGGAACAGGATTCATGAT 2823
QY 921 ThrAlaValArgSerIleAspProSerPheMetAsnLysTyrIleArgLysGlnCysGly 940
Db 2824 ACAGCAGTTCGGAGATTCATCTCTCTTATGAATTAAGTGAATTCGGAACAAATCGCA 2883
QY 941 IleGluAspGlnLysLysSerLysLysAspSerThrLysAsnProIleGluLysLys 960
Db 2884 ATTGAAGTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2943
QY 961 IleAspAsnThrGlnAlaMetLysLysTyrPheGlnLysValAspArgPheLeuTyrSer 980
Db 2944 ATTGATTAATCTCAACCCAGTGAAGAAATATTTTGAAGTGAATTCATTAATCTG 3003
QY 981 CysValGlyTyrSerValAlaThrTyrIleMetGlyIleLysAspArgHisSerAspAsn 1000
Db 3004 TGTGTTGATTAATTCAGTTCGCAAGTACATTAATGGGATTAAGGATTCGACATGATTAAT 3063
QY 1001 LeuMetLeuThrGlnAspGlyLysTyrValHisIleAspPheGlyHisIleLeuGlyHis 1020
Db 3064 CTGATGCTCACTGAAGATGGAATAATATGTCACATTTGATTCGTCACATTTTGGGACAC 3123
QY 1021 GlyLysThrLysLeuGlyIleGlnLysArgAspArgInProPheIleLeuThrGlnHisPhe 1040
Db 3124 GAAAGACCAAACTGGGATCCAGCAGAGTCGTCAACCGTTATTTCTAAACCAACCTTT 3183
QY 1041 MetThrValIleArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPhe 1060
Db 3184 ATGACAGTGAATTCGATCGGTAATCTGTGATGGAATTCGCAATGAGCTACAAATTC 3243
QY 1061 LysThrLeuCysValGlnAlaTyrGlnValMetTyrAsnAsnArgAspLeuPheValSer 1080
Db 3244 AAAAGTATGCGTGAAGCTTACGAAAGTAATGTGAATATCGAATTTGTTCTTTCC 3303
QY 1081 LeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrLysAlaAspLeuAsp 1100
Db 3304 TTGTCACCTTGATCTCGAATGGAATGCTGCTGAGCTGTTCAGCAAAACCGGATTTGAT 3363
QY 1101 HisLeuLysThrLeuPheCysAsnGlyGluSerLysGluGlnAlaArgLysPhePhe 1120
Db 3364 CATTGAAGAAACCTCTTCTGCAATGAGAAACCAAGAAAGGAGAAAGTTTTC 3423
QY 1121 AlaGlyIleTyrGlnGlnAlaPheAsnGlySerTyrPheSerThrLysThrAsnTyrLeuPhe 1140
Db 3424 GCTGCAATCTACGAAGAACCTTCAATGATGATGCTTACCAAAACGAATTTGCTTTC 3483
QY 1141 HisAlaValLysHisTyr 1146
Db 3484 CACGAGTCACCACTAC 3501

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US-10-027-591-1
; Sequence 1, Application US/10027591
; Patent No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADDU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
; US-10-027-591-1

Alignment Scores:
Pred. No.: 7,98e-111 Length: 5220
Score: 1033.00 Matches: 328
Percent Similarity: 43.76% Conservative: 194
Best Local Similarity: 27.49% Mismatches: 457
Query Match: 17.09% Indels: 214
DB: 9 Gaps: 41

US-08-908-453-1 (1-1146) x US-10-027-591-1 (1-5220)
QY 8 ProGlnLeuGlnThrMetValGlnGlnIleProGlnMetArgGluArgProSerLeuGlnThr 27
Db 202 CCTGGCGTGAAGTCCGCCATGGAATTCGACCAAGAGAAATCAAGACCTT----- 255
QY 28 GluAsnGlyLysGlySerLeuLeuGlnGluAsnGlyValAlaAspIleIleThrMet 47
Db 256 -----GTGGTTGACTTC-----CTG 270
QY 48 CysProPheGlyGlnValIleSerValValPheProTyrPheLeuAlaAsnValArgThr 67
Db 271 CTGCCACAGGAGGTCTTACTGAAC-----TTCCCT-----GTG 303
QY 68 SerLeuGlnIleLysLeuSerAspPheLysHisGlnLeu-----PheGln 82
Db 304 TCCGCCAATGCCAACCTTCAACCACTCAAGCAGCTGTGTGGACCGGCCAGATGAG 363
QY 83 LeuIleAlaProMetLysTyrGlyThrTyrSerValLysProGlnAspTyrValPheArg 102
Db 364 CCGCTCTTCCACATCTCAGTGGC-----CCGAGGCTATGTGTTCAAC 408
QY 103 GlnLeuAsnAsnPheGlyGlnIleGlnValIlePheAsnAspArgGlnProLeuSerLys 122
Db 409 TGCATCAACCAAGACAGCGGACGACGAGAGGTG-----GAGGAGACCAACGCGGTCTG 462
QY 123 LeuGlnLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArg 142
Db 463 TGTACATGACAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
QY 143 AspLysGlnLeuMetSerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGln 162
Db 523 AAGAAATCATCACTCAACATCAGCTCTCTCACTGCGCAAGGCTCCAGAGTTTGAC 582
QY 163 GluSerLeuAspGlnGlnIleuArgGlnPheArgAlaSerLeuTyrAlaArgThrLysLys 182
Db 583 TCTTTGTCGACCCAGGAAGTGAACGATGCTGCGCAAGAGTGCCTCAATTTCTCCAGAG 642
QY 183 ThrCysLeuThrArg-----GlyLeuGlnGlyThrSerHisTyrAlaPheProGln 199

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[illegible][illegible]

QY	871	Valmetxspapaniiaetpbyalalalasnlielapscyscybleasnprotyralalaval	890
Db	2581	CTCATGACGCTCTGTGAGACAGAGAGGGGCTGACCTGAGAGATGACCCCTTAGGCTGC	2640
QY	891	LeubProwetgijumetilegilyleilegivalvalProasmCyblyeThriIlephe	910
Db	2641	CTCCCAACGGGACCGCACAGGCGCTCATTTAGGGTGAACTCGGTTGACACCATGACC	2700
QY	911	GlulilegivalgilythrglyPheMetCasnThrAlaValAgSerIleasPProserPhe	930
Db	2701	AACCTCAACCTCAACAAGACCAATG---CGAGCCACAGCGCGCTTCACACAGATGCC	2757
QY	931	MetxanlystrPILeatsrglyGlnCyseglylegilaepgildulylylelyserlyelys	950
Db	2758	CTGCTCAACGTGCTGAG-----	2775
QY	951	AspSerThriyAsnProIleglululylylealeapnhringlAlaMetlybelyr	970
Db	2776	-----TCCAGAACCGCGGGGAG---GCCCTGAT-----	2802
QY	971	PhegluSerValaPaPaPheLeuTySerCyValGlyTySerValAlaThrTyIle	990
Db	2803	---CGACCCATYAGAGATTACCCCTCCGTGCTGGCTATTGTGTGCCACATATGTG	2859
QY	991	MetGlyIlelyAsPaPaTgHISerAsPaSnMetLeuThrGluAspGlyIleTyGVal	1010
Db	2860	CTGGGCGATTGGCGATTCGCGACAGACACACATCATGATCCGAGAGAGTGGGACGTGTC	2919
QY	1011	HISleleapPhegllyHISleleuglyHISgllyThryThrylsleuglyIleGlnaTasp	1030
Db	2920	CACATTGATTTGGCCACTTTCGGGGAAATTTCAAAGACCAAGTTTGGAAATCAACCGGAG	2979
QY	1031	ArgGlnProPheIleLeuThrglnHISPheMetThrValIleAgSerGlylySerVal	1050
Db	2980	CGTGTCCCATTCATCCCTCACTTATGACTTGTTCATGTGATTCAGCATGGACAGGGAAAGACT--	3036
QY	1051	AspGlyAsnSerHISgluluglyHISlyPheThryLeuCyValGluAlaTyGluVal	1070
Db	3037	---AATAATATGTAGAAATTTGAAACGGTTCCGGGCGTACTGTGAAGGCGCTTACCATC	3093
QY	1071	MetThryPasnAsnAArgApLeuPheValISerLeuPheThryLeuMetLeuglyMetGluLeu	1090
Db	3094	CTGGGGCGGCCACGGGCTTCTCTCTCCACTTTCGCCCTGAGTGGCGGCGGACAGCGCTG	3153
QY	1091	ProGluLeuSerThryValaAspLeuAspHISleuTySthThryLeuPheCyAsnGly	1110
Db	3154	CTGAGCTCAAGCTGCTCCAAAGACATCCAGATATCCAAAGACTCCCTG--GCACTGGGG	3210
QY	1111	GluSerTySglGluAlaArglyPhePheAlaGlyIleTyrgluGluAlaPheAsnGly	1130
Db	3211	AAAACAGAGAGAGGACCTGACATGACACTTCGAGAGAGTTTAACGAAAGCCCTCCGTGAG	3270
QY	1131	SerTySerThrylySthAsnTyPLeuPheHISAlaVal	1143
Db	3271	AGCTGGAACCAAGTGAACTGGCTGGCCACACAGCTG	3309
RESULT 4			
US-10-162-160-2			
Sequence 2, Application US/10162160			
Publication No. US20030099627A1			
GENERAL INFORMATION:			
APPLICANT: Van Hasebroeck, Bart			
TITLE OF INVENTION: No. US20030099627A1el Lipid Kinase			
FILE REFERENCE: 2332-1-002			
CURRENT APPLICATION NUMBER: US/10/162,160			
PRIOR FILING DATE: 2002-06-03			
PRIOR FILING DATE: 1998-12-01			
PRIOR APPLICATION NUMBER: 9611460.8			
PRIOR FILING DATE: 1996-06-01			
NUMBER OF SEQ ID NOS: 6			

; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 3387			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-162-160-2			
Alignment Scores:			
Pred. No.:	6,53e-111	Length:	3387
Score:	1031.00	Matches:	328
Percent Similarity:	43.59%	Conservative:	192
Best Local Similarity:	27.49%	Mismatches:	459
Query Match:	17.05%	Indels:	214
DB:	9	Gaps:	41
US-08-908-453-1 (1-1146) x US-10-162-160-2 (1-3387)			
Qy	8	ProGlnLeuGlnThrMetValGlnGlnTrpGlnMetArgGluArgProSerLeuGluThr	27
Db	7	CTGAGGGGTGACGCGCCCATGAAATTCGACCAAGAGGAAATCAGAGCTT-----	60
Qy	28	GluAsnGlyValSerLeuLeuLeuGlnGlnGluValAlaAlaSerIleIleThrMet	47
Db	61	-----GTGGTGAAGCTTC-----CTG	75
Qy	48	CysProPheGlyGluValIleSerValAlaPheProTrpPheLeuAlaAsnValArgThr	67
Db	76	CTGCCACAGGGGTCTACTGTAAC-----TTCCCT-----GTG	108
Qy	68	SerLeuGluIleLeuSerAsnPheLeuSerIleLeu-----PheGlu	82
Db	109	TCCCGAATGCCCACTCAGACCATCAAGCAGCTGTGTGGACCGCGCCCACTATGAG	168
Qy	83	LeuIleAlaProMetLeuTrpGlyThrTrpSerValLysProGlnAspTrpValPheArg	102
Db	169	CCGCTCTTCCACATGCTCAGTGGC-----CCGAGGCGCTATGTGTTCAAC	213
Qy	103	GlnLeuAsnAsnPheGlyGluIleGluValIlePheAsnAspArgLysProLeuSerLys	122
Db	214	TGCAATCAACCAAGCAGCGGAGCAGCAAGACTG-----GAGGACGAGCAACGGCGCTG	26
Qy	123	LeuGlnLeuHisGlyThrPheProMetLeuPheLeuTrpLysProAspGlyIleAsnArg	142
Db	268	TGTGAGGTGAGCGCTTCTGCGCGCTGCGCGCTGTGGCGCCGCGAGGCGCACCGCGTG	327
Qy	143	AspLysGlnLeuMetSerAsnIleSerHisCysValLeuGlyTrpSerLeuAspLysLeuGlu	162
Db	328	AAGAACTCATCACTCAACACAGATGACCTCTCATCGGCAAAAGCGCTTCCAGACTTGAC	387
Qy	163	GluSerLeuAspGlnGlnLeuArgLysPheArgAlaSerLeuTrpAlaArgThrLysLys	182
Db	388	TCCTTGTGCAACCCAGAGTGAACCACTTTGGCGCCCAAGATGTGCCAATTTGTGGAGAG	447
Qy	183	ThrCysLeuThrArg-----GlyLeuGlnGlyThrSerHisTrpAlaPheProGlu	199
Db	448	GCGGCGCGCGCGGAGCAGCTGGGCGGAGGCGCTGGCTGCAGTACAGTTTCCCGCTG	507
Qy	200	GlnGlnTrpLeuCysValGlyLysSerCysProLysAspLeuGlnSerLysValLysAla	219
Db	508	CACCTGAGAGCCCTCGGCTCAAACTGGGGGCGCTGTACCTCGCGACTCCGACCGGGCC	567
Qy	220	AlaLysLeuSerTrpGlnMetPheTrpArgLysArgLysAlaGluIleAsnGlyValCys	239
Db	568	CTTCTGTGTCAAC-----GTTAAGTTTGAAGGC--AGC	597
Qy	240	GlyLysMetMetLysIleGlnIleGluPheAsnProAsnGlnTrpLysSerLeuLys	259
Db	598	GAGGAAAGCTTCACTTCCAGGTG-----TCCACCAAGAGCAGTCCGCTGGCCGCTGATG	651
Qy	260	HisThrPheLeuTrpGluMetArgLysLeuAspValTrpArg-----ThrAspAsp	276
Db	652	GCGTGTGCGCTG-----CGAAGAAAGGCAACAGTGTTCGCGGACCGCGTGTGGACAG	705


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Db      2581 -----TCCAGAACCCGGGGAG---GCCCTGAT-----2607
Qy      971 PheGUSerValAspArgPheLeuTySerCyValGlyTyrSerValAlaThrTyrIle 990
Db      2608 ---CGAGCATTTGAGAGATTACCTCTCTGCTGCTGCTATGTTGTCACATATG 2664
Qy      991 MetGlyIleTyAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyTyrVal 1010
Db      2665 CTGGCATTTGGCGATCGGACACGACCAATCATGATCCGAGAGAGTGGAGCTGTC 2724
Qy      1011 HisIleAspPheGlyHisIleLeuGlyHisGlyTyrValLeuGlyTyrIleGlnArgAsp 1030
Db      2725 CACATTGATTTTGGCCACTTCTCTGGAATTTCAAGACCAAGTTGGAATCAACCGCGAG 2784
Qy      1031 ArgGlnProPheIleLeuThrGluHisPheMetThrValIleArgSerGlyTyrSerVal 1050
Db      2785 CGTGTCCATTCATCTCATCTACAGACTTGTCTCATGTGATTCACAGAGGAGAGCT-- 2841
Qy      1051 AspGlyAsnSerHisGlyLeuGlnIleTySerPheLeuTySerValGluValTyrGluVal 1070
Db      2842 ---AATAATAGTGAAGAAATTGACGCTTCGGGGCTACTGTGAAGGCTTACACATC 2898
Qy      1071 MetTrpAsnAsnArgAspLeuPheValSerLeuPheThrLeuMetLeuGlyMetGluLeu 1090
Db      2899 CTGGCGCCGCCACGGGCTTCTCTCTCCACCTCTTGGCCCTGATCGGGCGGACAGGCTTG 2958
Qy      1091 ProGluLeuSerThrValAlaAspLeuAspHisIleLeuTySerValLeuPheCysAsnGly 1110
Db      2959 CTTGAGCTGCTGCTCTCCAAAGACATCCAGATCTCAAGAGACTCCTG--GCACTGGGG 3015
Qy      1111 GluSerTySGluGluAlaArgIlePhePheAlaGlyIleTyrGluGluAlaPheAsnGly 1130
Db      3016 AAACAGAGAGAGAGAGCATGAGACATTCGAGGAGAGTTAAAGAGAGCTCCCTGAG 3075
Qy      1131 SerTrpSerThrTyThrAsnTrpLeuPheHisAlaVal 1143
Db      3076 AGCTGAAACCAAGTGAAGTGGCTGGCCCAACAGTG 3114

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RESULT 5

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US-09-917-800A-477
; Sequence 477, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Caetle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917, 800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patent In Ver. 2.1

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; SEQ ID NO 477
; LENGTH: 5990
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477

Alignment Scores:
Pred. No.: 1.7e-67 Length: 5990
Score: 668.00 Matches: 270
Percent Similarity: 40.29% Conservative: 153
Best Local Similarity: 25.71% Mismatches: 388
Query Match: 11.05% Indels: 240
DB: 10 Gaps: 40

US-08-908-453-1 (1-1146) x US-09-917-800A-477 (1-5990)
Qy      202 TyrLeuCyValGlyGluSerCyAspProIleAspLeuGluSerTyValIleAlaIaIys 221
Db      1067 TTTATGTCAATATGATGACAGCTTCCCAAGAGATCTTCAAG-----1111
Qy      222 LeuSerTyGlnMetPheTrpArgIys-----ArgIysAlaGluIleAsnGlyValCys 239
Db      1112 -----TATATGCGGCTCTG-AGGAATTTTACAGACGATCACTCTAGGAGACCA 1164
Qy      240 GluTyMetMetIleIleGlnIleGluPheAsn-ProAsn-----GluThrProIysSe 252
Db      1165 AATATTTTCAGAAAGTAATCTGTCAATTCATCTCCAGAGAAAGACGAGACATC 1224
Qy      253 -----1225
Db      1225 CAGGAATTTATCCCGAAGAGGATGATGACCGGATCGGCTCATCTGAACCAATTC 1284
Qy      257 rLeuLeuHisThrPheLeuTyGlnMetCArgIysLeuAspValTyrAspThrAspAspPr 277
Db      1285 TAGAATTTACATATTTGGAATAATATACAGACATGCTCTCCACAGTAAATGAAG-- 1342
Qy      277 AlaAspGluGlyTrpPheLeuGlnLeuAlaGlyArgThrThrPheValThrAsnProAs 297
Db      1343 -----CTACAACTCCATGTCGACACCT--GTTGAAAAACCCAGG 1380
Qy      297 pValIleLeuThrSerTyTrpAspGlyValArgSerGluLeuGluSerTyArgCysProG 317
Db      1381 A-----AGATGTGGAG 1392
Qy      317 yPheValValArgArgIleSerLeuValLeuIleAspTyrCysArgProIysPro----- 335
Db      1393 A-----GAACTCTGTCATCATGTTTCTGTCGCGACACCTCTC 1437
Qy      336 -----LeuTyGluProHisTyrValArgAlaHisGlyArgIysLeuAlaLeuAspVal 354
Db      1438 AGCCACATGGGAATGACATTTATGAAATGTAGAAATATGACAGTCTTCGGGGTGA 1497
Qy      354 u-----SerValSerIleAspSerThrProIysGlnSerTyAsnSerAspMetValMe 372
Db      1498 TTGAACCAACCAAGATTCAATGCAATGAAAGAACTAATCTTATTTGCGAGAACCAT 1557
Qy      372 tThrAspPheArg-----ProThrAlaSerLeuIleGlnVal-SerLeuTrpAspLeu 390
Db      1558 CACGAAATTTTCATCAGATTCAGAGACTTCAAAAAAGGCTTCATAGAAAGTGCAT 1617
Qy      1618 CGGAATCTGAGATCCCTCATCATGAGCTTGAAGTGAATGACGATGAGCTTTTATACG 1677
Db      1678 AT-----TTCCGGCTGCGCGCGACCTGAGGGGCTCTCCGCCACACGCTG 1725
Qy      410 spMetTyValArgIleGluPheSerVal-----419
Db      1726 GGCTCACTCCACCTAGCTTACAGGAGTGTCTCCCTGACAAATGTTCAGAACTGGG 1785

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QY 420 -----TyrValGlyThrLeuThr 426
 Db 1786 CACAGACTACAAAGCATTTTCATTTCTCTGCTGCATCATATGCTGGAAAGAGCTGT 1845
 QY 426 euaLaserlyser-----ThrThryValAsnAlaGlnPheAlaIysT 441
 Db 1846 GCCAAGTAAAGCTGCAGATCCCTGCCAGTCAAAAGCATCTCTTTTGGGGAAT 1905
 QY 441 rPAsnlysgLumetyrThrPheAspLeuTywelysAspMetProProserAlaValL 461
 Db 1906 GGAAT---GAAATATCAATTTTCTTGAGATAAAGCATCTCCAAAGAGATCATGC 1962
 QY 461 euSerlleKrgValLeuTyrglyValylsLeuLysSerGluGlnPheGluValGlyT 481
 Db 1963 TCGTATATAAG---CTGTTGGATTGACAGTCCACCCAGCCGAATCTGCGCT 2019
 QY 481 rPValAsnMetSerLeuThrAspTrpArgAspGluLeuArgGlnGlnPheLeuPhe 501
 Db 2020 GGACCTGCCTTCACATTT----- 2039
 QY 501 iLeuTrpAlaProGluProThrAlaAsnArgSerArglleGlyGluAsnGlyAlaArgI 521
 Db 2040 -----CCAAAAGAAAGCTCCGCTGGGGTCTAGCTTCTCAGCA 2079
 QY 521 lleGlyThrAsnAlaAlaValThrIleGluIleSerSerTyrgly-----GlyArgV 538
 Db 2080 TTAACACTACAGAGTGCCTCTATAGAAATAGTGGCTCCAGAGATAGAGATGGAGGCC 2139
 QY 538 aArgMetProSerGlnGlyGlnTygThrTyrlleuValylsHisArgSerThrTrp--- 556
 Db 2140 AACCTAACCCACTGAGCCCTGATAGATTTT-----CCAGTGCACCTGGGAGT 2190
 QY 557 -----ThrGluThrLeuAsnIleMetGlyAspAspTyrglu-----SerCysI 571
 Db 2191 AGCTGAACCTGAGACTGAAAGAAACAGAACTGACACCAAGAGCCTCCAAAGAGATGT 2250
 QY 571 laArgAspProGlyTyrglyValylsLeuGlnMetLeuValylsHisGlnSerGlyIleV 591
 Db 2251 TA-----AAACACATCGCAGACTCTCCAAAAG---CAGCTCCCTTC 2292
 QY 591 alleuGlnGluAspGlnGlnArgHisValTrpMetTrpArgTyrglyIleGlnTygGln 611
 Db 2293 TACTTCTGTGGAAGAGAGATATTGTGGTTTATGCTTCTCTACCAACAAGAGA 2352
 QY 611 lUpProAspLeuLeuIleValLeuSerGluLeuAlaPheValTrpThrAspArgGluAsn 631
 Db 2353 ACTCTCTCTCCCTCTGCTCTGGGAGC---GCCCTCGTGG---GATGAAGGAGCAG 2406
 QY 631 heSerGluLeuTyrglyValMetLeuGluTyrglyAspProProserAlaAlaAlaLeuT 651
 Db 2407 TTTTGGAAATGCAATGCCGCTTGAGAAAGGAGCATTTTCCATCCGTTGAAAGCTCTTG 2466
 QY 651 hTrLeuLeuGlyLysArgCysThrAspArgValIleArgLysPheAlaValGluTyLeuA 671
 Db 2467 GCCTTTTGACTTCAGATTTCCAGACCAAGACATGTGTAAGTTGACGTTCAACACTTGG 2526
 QY 671 snGluGlnLeuSerProValThrPheHisLeuPheLeuPro---LeuIleGlnAla 690
 Db 2527 ACAACTCTTGACCCGATGAGCTG---CTGAGCTGCCTCCCAAGCTAGTTCAGGCTG 2580
 QY 690 euLysTyrgluProArgAlaGlnSerGluValGlyMetLeuLeuThrArgAlaLeu 710
 Db 2581 TCAAGTTTGAAGTGTGAGTCTGAAAGTCCCTTGATGAACTCCGCTTTCATCGATCCCTTG 2640
 QY 710 yAspTyrglyArglleGlyHisArgLeuPheTrpLeuLeuArgAlaGluIleAlaArgLeuA 730
 Db 2641 AAAGACTCGAGTGGCTCACCCGCTGTCTGCTGCTGGG----- 2681
 QY 730 rGAspCysAspLeuLysSerGluGlnTyrglyArglle-----SerLeuLeuMetC 747
 Db 2682 -----GATGACCAAGGTGAAGACTATTAAAGCTGTGACAGAGACTTTTGGCGC 2733

QY 747 lUaIaTyrlleuArgGlyAsnGluGlnHisIleLysIleIleThrArgGlnValaAspMetV 767
 Db 2734 CTCTCAGTTCTGTGCAGAGAAAGCCCTGATGTAAGAGCTTTCAAAGCAGAAACTTG 2793
 QY 767 aLAspGluLeuThrArglleSerThrLeuValyls-----GlyMetProLysT 783
 Db 2794 TCAACTCCTGGGTGATATTGAGAAAGAGAAAGTGGCTGCGATGCTCAGAGAAAGG 2853
 QY 783 rPValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsnM 803
 Db 2854 ATGTG-----CTAAAGAGAGATTTGGAGCTGTGAGAAAGATTTCTTTAAAGATA 2901
 QY 803 eAspSer-----ProLeuAspProValTyrglyLeuGlyGlyMetIleIleAspL 820
 Db 2902 TTAACACTTGCATCTTCTCTGAACCCGCGCTGTGGCTAAAGAGATTAACGGAGTG 2961
 QY 820 yAlaAlaIleValLeuGlySerAlaLysArgProLeuMetLeuHisTrpLysAsnLysAsn 840
 Db 2962 CATGTCATATTTCATCTAATGCTTGCCTTGCATGAAATCATCTTTCATCAATGCTAATC 3021
 QY 840 rOlySerAspLeuHisIleuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuA 860
 Db 3022 CAATGGC-----AAAAATACAGGTATTATTTAAAGCCGCGCAGATCTTC 3069
 QY 860 rGlnAspMetLeuValLeuGlnValaIleMetAspAsnIleTrpLysAlaAla 880
 Db 3070 GGCAGAGATATGCTTTCTGCAATATTCATCAAGTATGACACACTTGGCTTCAGAGG 3129
 QY 880 snIleAspCysAspLeuAsnProTyrglyAlaValaIleuProMetGlyGluMetlleGlyIleI 900
 Db 3130 GCCTGATATGCAATGATCATTTATGATGCTGACCAAGAGAAAGCCTCAAGATTTCA 3189
 QY 900 lleGlnValaIleProAsnGlyLysTrpIlePheGlnIleGlnValaGlyThrGlyPheMetA 920
 Db 3190 TAGAGATGGTGGCTTATGCTGTAAAGCTTGGCCAAATCATTTGACTGGGCTG--- 3245
 QY 920 snThrAlaValaArgSerlleAspProSerPheMetAsnLysTrpIleArgLysGlnCysG 940
 Db 3246 -----ATAGAGACCCCTGAAAGAAACACCATCAAGAAAGCTTC----- 3284
 QY 940 lYlleGluAspGluLysLysLysSerLysLysAspSerThrLysAsnProIleGluTyL 960
 Db 3285 -----AGTCAGACCAACCATTAAGAGATTTGAAAGG 3321
 QY 960 yAlleAspAsnThrGlnAlaMetLysLysTyrglyPheGluSerAlaAspArgPheLeuTyS 980
 Db 3322 CCTGAGGAC-----TTTTTTTACT 3342
 QY 980 eFCysValGlyTyrlserValAlaThrTyrlleMetGlylleLysAspArgHisSerAspA 1000
 Db 3343 CTGTGTCTGGCTGGTGTGTGTGTGACATTCATCTTGGAGTCTGTACCGACATATAGACA 3402
 QY 1000 snLeuMetLeuThrGluAspGlyLysTyrglyAlaHisIleAspPheGlyHisIleLeuGlyH 1020
 Db 3403 ATATCATGCTGACAAAGTCAAGCCACACATGTTCAATTTGAAATTTCTTGGGCTC 3462
 QY 1020 iGlyLysThrTyrlleuGlylleGlnArgAspArgGlnProPheIleLeuThr----- 1037
 Db 3463 ACGCAACAACTTTGGCGGTATTAATAAGGACCGAGCGCTTTCATTTTACTTTCAGAGA 3522
 QY 1038 --GluHisPheMetThrValIleArgSerGlyLysSerValaAspGlyAsnSerHisGluL 1057
 Db 3523 TGGAGTACTTTATTCG-----GAGCGTGGAA-----AACACAGAGCATT 3564
 QY 1057 euGlnLysPheLysThrLeuCysValaGluAlaTyrglyValaIleTrpAsnAsnArgAspL 1077
 Db 3565 TTCAGACTTCTGGAACCTGCTCAGAGCCTCAACAATTTGTGAAGAGCACACCAAC 3624
 QY 1077 euPheValSerLeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrLysA 1097
 Db 3625 TCTCTGTAGCTTTTCAAGAAAGATGCTGATCCGCGGCTTCTTCAAGCTGAGAGGGGATTG 3684
 QY 1097 laAspLeuAspHisLeuLysLysTrpLeuPheCysAsnGlyLysLeuSerGluGluAla 1117

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Db      3665 AAGACCTGAATACTACGACGACAAATCTCCGCGCAAGACAGACAGCTGAAGCCACAA 3744
Qy      1117 rglvPhePhehlaelylylrygu-----gluAlaPhehseNglYserTpsertHl 1135
Db      3745 GTCATTATTCACGAGATTAAGCAGAGCTGTGAGTGTCTTC-----CCAGTTA 3792
Qy      1135 ysthrAsenTrrleuphehIsalaval 1143
Db      3793 AACTGAATTAACCTGATCCACAGCTT 3818

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RESULT 6

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US-10-092-219-1
; Sequence 1, Application US/10092219
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Domlin, Jan
; TITLE OF INVENTION: No. US2002015114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

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Alignment Scores:

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Pred. No.: 2,076-62 Length: 5061
Score: 624.00 Matches: 207
Percent Similarity: 45.44% Conservative: 122
Best Local Similarity: 28.59% Mismatches: 301
Query Match: 10.32% Indels: 94
DB: 12 Gaps: 24

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US-08-908-453-1 (1-1146) x US-10-092-219-1 (1-5061)

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Qy      440 LysTPAenLysGLMetTyThrPheAspLeuTyRmeLysAspMetProPseSerAla 459
Db      2218 AAATGGGAT--GAACCTAATCTTTTCTTATCCAGATATTCACAATGGCCATTAGAAATCA 2274
Qy      460 ValLeuSerIleArgValLeuTyRglYlySval----- 470
Db      2275 GTTCTTCACTT--ACTCTTTTGGAAATTTAAATCAGACAGCGAAGTTCCCTGAT 2331
Qy      471 -----LysLeuLysSerGluLubhegluValGlyTPValAsmMetSerLeuThrAsp 488
Db      2332 TCTAATAAGCAGAGAAAGGAGCAGAGAGCTTTGGCAAGTTCTTACCTCTTTGTGAC 2391
Qy      489 TrpArgAspGluLeuArgGlnGlyGlnPheLeuPheHIsleuTPAlaProGluProThr 508
Db      2392 TTTAGACGGTTTAAACATGCGAAGCTTAACCTTCTAATCTTTGAGCTTCATCACAATACA 2451
Qy      509 AlaAsnArgSerArgIleGlyGluAsnGlyAlaArgIleGlyThrAsnAlaAlaValThr 528
Db      2452 -----AATCTGTTCCGGAACGTTACCAAAAAGGA 2484
Qy      559 IleguIleSerSerTyRglYglYArgValArgMetProSerGlnGlyGlnTyRThrTyR 548
Db      2485 TATGTCATGAAGAAATAGTGTCTACAGAGTGAATTTCTTCTCCCT-----GCATTT 2535

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Qy      549 LeuValIleHIsArgSerThrTrpThrGluThrLeuAsnIleMetGlyAspAspTyRglu 568
Db      2536 GATATTATTATTAACACTCTCCATAGTACAGAAACATTTATACAGAACTATCAATTAAGA 2595
Qy      569 SerCySillArgAspProGlyTyRlyLysLeuGlnMetLeuValIleYlser 588
Db      2596 ACACTAGAGAAATGATATTAAGGGAACCTCTGATATCTTCATATAA-----GACTCA 2649
Qy      589 GlyIleValLeuGluLubAspGluGlnArgHIsValTPMetTrpArgTyRtllegln 608
Db      2650 TCATCTGACCTTTCTTAAGAAAGATTAACCTTTTATGAGAG--AAACGTTATATTGTC 2706
Qy      609 LysGlnGluProAspLeuLeu-----IleValLeuSerGluLeuAlaPheValTrpThr 626
Db      2707 TTCAAAACACCAAAATGCTCTTCTTAATATTTAGAACAGCCGCCAACTGAAATGCG--- 2763
Qy      627 AspArgGluAsnPheSerGluLeuTyRValMetLeuGlnTyRTPRysProPseSerVal 646
Db      2764 -----GGTAATCTTGCAGAAACCTTACATGCTTCCACAGTGGCCTGCATTTGACCA 2817
Qy      647 AlaAlaAlaLeuThrLeuGlnGlyYlArgGlySerThrAspArgValIleArgYshehla 666
Db      2818 CTAAATGCAATGGAACCTTCTTGATTCAAAAATTTGCTGATCAGGAAGTAAGATCCCTAGCT 2877
Qy      667 ValGluYsLeuAsnGluGlnLeuSerProValThrPheHIsleuPheIleuProLeu 686
Db      2878 GTGACCTGGATT--GAGGCCATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2934
Qy      687 IleglnAlaLeuTyRglYgluProArgAlaGlnSerGluValGlyMetMetLeuThr 706
Db      2935 GTACAGCTTGAATATGAATGAATTTACTGAATGATTCATTAGTCAATTCCTTTTGCC 2994
Qy      707 ArgAlaLeuCyAspTyRArgIleGlyHIsArgLeuPheTrpLeuAlaAlaIle 726
Db      2995 AGGGCATTGGGAATATCCAGATAGCACAATTTATATGCTTCTCAAA----- 3045
Qy      727 AlaArgLeuArgAspCyAspLeuLysSerGluGluTyRArgArgIle-----SerLeu 744
Db      3046 GATGCCCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3102
Qy      745 LeuMetGlnAlaTyRLeuArgGlyAsnGluGlnHIsIleYlIleThrArgGlnVal 764
Db      3103 CTGTGACGAGGAGGAGAAACGACTTAGAGAGAAACCTTCAAAA-----CAGACG 3150
Qy      765 AspMetValAspGluLeuThrArgIleSerThrLeuValYs-----GlyMetPro 781
Db      3151 AAACCTGTACAGCTTTTAGAGAGAGTACAGAAAAAGTAGACAGCAGTAGAGATCAGACC 3210
Qy      782 LysAspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHIsIleMetGlu 801
Db      3211 AGACAGGTTGTTTCCAAAGAAAGTAGAGAGAGTACAGTCTTTTTCAGAAA---AAT 3267
Qy      802 AsnMetAspSerProLeuAspProValTyRlySleuGlyGlnMetIleIleAspYsAla 821
Db      3268 AAATGCCGTCCTCCCTCAACCAAGCTAGGCAAAAGATTAATTAATTAATTAATTAATTAAT 3327
Qy      822 IleValLeuGlySerAlaYlArgProLeuMetLeuHIsTrpYsAsnYlAsnProYs 841
Db      3328 TCCTTCTTCACTTCAATGATGCTGCTCCCTTAAGGCAATAGTGAATGCTGACCTCTG 3387
Qy      842 SerAspLeuHIsleuProPheCyAlaMetIlePheYsAsnGlyAspAspLeuArgGln 861
Db      3388 GGAGAA-----GAAATTAATCATGTTTAAAGGTTGGTGGAGAACTTTCGGCA 3435
Qy      862 AspMetLeuValLeuGlnValLeuGlnValMetAspAsnIleTrpYsAlaAlaAsnIle 881
Db      3436 GATATGTTAGCTTTAAGATATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3495
Qy      882 AspCySylAsnProTyRAlaValLeuProMetGlyGlnMetIleGlyYlIleleu 901
Db      3496 GATCTGAGATGATGATTAATTTTCAAAATGCTTCAACCTGCAAGATCGAGGATGATGAG 3555
Qy      902 ValValProAsnCySylThrIlePheGluIleGlnValGlyThrGlyPheMetAsnThr 921

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Db      3556 CTGGTTCCTCGTCCGATACCTTCAGAAAATCCAGTGAATATGCT----- 3603
Qy      922 AlAlaValArgSerIleAspProSerPheMetAenlys-----TriPleArglys 937
Db      3604 -----GTGACAGAGATCCTTTAAAGATAAACCACTTGACAGATGGCTTAAGAAA 3651
Qy      938 GlncysGlyIleGluAspGlyIleValysSerIleValAspSerThrIleAsnProIle 957
Db      3652 TAC----- 3663
Qy      958 GluIlyIleAspAsnThrGlnAlaMetIlyIlePheGluSerValAspArgPhe 977
Db      3664 GAA-----GAAGATATGAAAAGGCTTCAGAGAACTT 3696
Qy      978 LeuTySerCysValGlyTySerValAlaThrTyIleMetGlyIleLysAspArgHis 997
Db      3697 ATCTATTCCTGTCGTGATGCTGTGTAGCCACTTATGAGCATCTGTGATCGACAC 3756
Qy      998 SerAspAsnLeuMetLeuThrGluAspGlyIleTyValHisIleAspPheGlyHisIle 1017
Db      3757 AATGACAAATATATATGCTTGAAGACACGAGACATGTTTCAATTCATCTTGAAGATT 3816
Qy      1018 LeuGlyHisGlyIleThrIleValGlyIleGlnArgAspArgGlnProPheIleLeuThr 1037
Db      3817 TTGGGACATGCACAGATGTTTGGCAGCTTCAAAAGGATCGGCTCTTTGTCGTGACC 3876
Qy      1038 GluHisPheMetThrValIleArgSerGlyIleValAspGlyIleAsnSerHisGluLeu 1057
Db      3877 TCTGATATGTCATATGCTTATATGCGGTGAAGAAG-----CCGACATTCCTTT 3927
Qy      1058 GluIlyPheIleThrLeuIleValGluAlaTyGluValMetTrpAsnAsnArgAspLeu 1077
Db      3928 CAGTGTGTGTGACCTCTGCTGTCAAGGCTTCACTTATTAAGAAACAGACAAACCTT 3987
Qy      1078 PheAlaSerLeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrIlySala 1097
Db      3988 TTTCTTAACCTCCTTCACTGATGATCTTCAAGGTTACCAAGATTTCAGATATCA 4047
Qy      1098 AspLeuAspHisIleValysIleThrLeuPheCysAenGlyIleSerIlyGluIleValArg 1117
Db      4048 GATTTCGAATATGCTTGAAGATGCATCAACCCCAA--ACTACACACGACAGAACTTACA 4104
Qy      1118 LysPhePheAlaGlyIleTyGluGluAlaPheAsnGlySerTrpSerThrIlyThrAsn 1137
Db      4105 ATTTCTTACTAGAGCTTATGATGATCAAGTTTG--GAAAGCATTCGCAAAAGTTTAA 4161
Qy      1138 TriLeuPheHis 1141
Db      4162 TTCTTCATTCAC 4173

RESULT 7
US-09-921-232-1
/ Sequence 1, Application US/09921232
/ Patent No. US20020102681A1
/ GENERAL INFORMATION:
/ APPLICANT: Martino-Cact, Susan J.
/ APPLICANT: Wang, Hongyu
/ APPLICANT: Beach, Larry R.
/ TITLE OF INVENTION: Polypeptides Controlling Phytate
/ FILE REFERENCE: 0706D4
/ CURRENT APPLICATION NUMBER: US/09/921,232
/ CURRENT FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/055,446
/ PRIOR FILING DATE: 1997-08-11
/ PRIOR APPLICATION NUMBER: 60/055,526
/ PRIOR FILING DATE: 1997-08-08
/ PRIOR APPLICATION NUMBER: 60/053,944
/ PRIOR FILING DATE: 1997-07-28
/ PRIOR APPLICATION NUMBER: 09/118,442
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: 09/677,064

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/ PRIOR FILING DATE: 2000-09-29
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 3252
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (258) ... (2666)
/ NAME/KEY: misc_feature
/ LOCATION: (1) ... (3252)
/ OTHER INFORMATION: n = A,T,C or G
US-09-921-232-1

Alignment Scores:
Pred. No.: 3,71e-54 Length: 3252
Score: 551.50 Matches: 200
Percent Similarity: 38.68% Conservative: 123
Best Local Similarity: 23.95% Mismatches: 297
Query Match: 9,128 Indels: 215
DB: 10 Gaps: 27

US-08-908-453-1 (1-1146) x US-09-921-232-1 (1-3252)
Qy      415 IlegluPheSerValTyValGlyThrLeuThrIleAlaSerIlySerThrThrIlyVal 434
Db      381 GTTGAGTGCAGACCTTATACATGATGATCCATTTGGGTTGCCCTTAACAAAGCTTG 440
Qy      435 AsnAlaGlnPheAlaLys-----TriPasnIlyMetTyThrPheAspLeuTyIleMet 452
Db      441 GAACCTTCGACCGAATATGCTTGAAT--GAGTCATATCAATTAACTACCAATATAC 497
Qy      453 LysAspMetProProSerAlaValLeuSerIleArgValLeuTyGlyIlyValysLeu 472
Db      498 AGGGACCTTACATCCCTCTCGCAGCTTCATTACGATG-----TGGAGTCTCATCT 551
Qy      473 LysSerGluGluPheGluValGlyTyValAsnMetSerLeuThrAspTrpArgAspGlu 492
Db      552 GGTGGAACCTCGAGGTTGTCGTTGACCCACCAATATTTCTTTTAACGACAAAGCGAG 611
Qy      493 LeuArgGlnGlyIlePheLeuPheHisLeuThrAlaProGlu----- 506
Db      612 CTTAAACAGAGAAGACAGAGCTGGGCTGGCCCAAAAGAGAGAGATGAGAGATC 671
Qy      507 ProThrAlaAsnArgSerArgIleGlyIleValysAla----- 519
Db      672 CCCACCACAACCTCTGCAAGGTTCTTAGATGAGAGGGGTGAGATGAAAGCTTGGAA 731
Qy      520 -----ArgIle 521
Db      732 AGCTTTGTTAACAGATATGACAGAGGACATACATGTTGATTGCTGATGCTT 791
Qy      522 GlyThrAsnAla----- 525
Db      792 GCCTTCAGCTATGAGCAAGCTATGAAAAAGGTGAGAGAGAGCAATTGTTC 851
Qy      526 ---AlaValThrIleGluIleSerTyGlyIleValArgValArgMetProSerGlnGly 544
Db      852 CCTAGCTCGGTGTGATGATGCAAGTTTGAACATGATGATGTTCTTCAGAAATCTGGA 911
Qy      545 GluTyThrTyLeuValIleHisArgSerThrTrpThrGluThrLeuAsnIleMetGly 564
Db      912 GCAAAATTTTATACACCGGCCCAATATCATTAATGAATGACTGTTACTGATAG--- 968
Qy      565 AspAspTyArgLysCysIleArgAspProGlyTyIlyValysLeuGlnMetLeuValys 584
Db      969 ---GACCCGGAAGCTTGAAGAAGCAATCATCTGACACAAAGCAGTTAAAGCTTCTAG 1025
Qy      585 LysHisGluSerGlyIleVal----- 591
Db      1026 ACCTTGACTCGTGGATGTTGATGATGATTAACCAAGCTCAAAATGAGAGAAAGTTA 1085

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QY 592 -----LeuGluGluAspGluGlnArgHis 599
 DB 1086 CTACAAACATATTAAAGTTTCCTCCTACAGCACCTGGAGATGAGAGAAATGG 1145
 QY 600 ValTyrMetTyrPargArgTyrIleGlnLysGlnLysProAspLeuIleValLeuSer 619
 DB 1146 GTGTGAAGATTTCGTTCTCTCTTGTGATGCTGAGAAAGAAAGCTTCAACGAAATTTCTCCGC 1205
 QY 620 GluLeuAlaPheValTyrThrAspArgLysPheSerGluLeuTyrValMetLeuGlu 639
 DB 1206 TCAGTGGAT-----TGGAGTATTAACCAAGAGCTTAACGAGCTGGTAGTGAATGGA 1259
 QY 640 LysTyrLysProProSerValAlaAlaIleLeuThrLeuGluLysArgCysThrAsp 659
 DB 1260 AAGTGGAAATGATGATGATGCTGATGACCTAGAGCTTCTCTCAGCTGATTTGAAAGC 1319
 QY 660 ArgValIleArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerProValThrPhe 679
 DB 1320 GACGAAAGTTCCGTGATGCTGCTCAGCGTACTT---GAAAGGGCTGATGATGAAATTA 1376
 QY 680 HisLeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGluProArgAlaGlnSerGlu 699
 DB 1377 CAGTCTATTTACTCTCAGTTAGTGAAGCTTTCGTTGAAAGATCTGACAAATGCCGT 1436
 QY 700 ValGlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgPhe 719
 DB 1437 CTAGCACTCTTCTTGAACCGCTCTTGTCTCAACATCGAAATGCTAGTCTCTCCGG 1496
 QY 720 TrpLeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluLysTyr 739
 DB 1497 TGGTATATATTAGTTAGTAG-----CTTCACAGTCTCTCAATAT 1532
 QY 740 ArgArg-----IleSerLeuLeuMetGluAlaTyrLeuArg----- 751
 DB 1533 GCACACCATATTATGACACATATGACATGCTTGAACACAGATGATGAATGGCTGGT 1592
 QY 752 -----GlyAsnGluGlnIleHisLeuSile-----IleThrArgGlnValAsp 765
 DB 1593 AGGAGAGATGGAGATGAGATGATTTGACCTGTGGACAGATTAAACCGGACAGACAG 1652
 QY 766 MetValAspGluLeuThrArgIleSerThrLeuValLysGlyMetProLysAspValAla 785
 DB 1653 CTCACGTCTCAATGCTGTCTATTATG-----AAGGATTAAGA 1691
 QY 786 ThrMet-----LysLeuArgAspGluLeuArgSerIle 796
 DB 1692 AATGTAAGAGTAGCCGCAAAAATAATGAAATAATGAGGACACTATATCAGAGATT 1751
 QY 797 SerHisLysMetGluAsnMetAsp-----SerProLeuAspProValTyrLys 812
 DB 1752 TTCAGTGAAGCTTACAACTTTGATGAGCCAAATGCTTACCACTTTCACCAACACTTCTC 1811
 QY 813 LeuGlyGluMetIleIleAspLysAlaIleValLeuGlySerAlaLysArgProLeuMet 832
 DB 1812 CTAAACGAGAGTTGCTCTCAAGAAATCGTCTATATTAAAGAGTGCCTTGAACCTTTGGCG 1871
 QY 833 LeuHisTyrLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIle 852
 DB 1872 CTGACATTAAACGCAAAATGGCCGACATCC-----AAGATTATTT 1913
 QY 853 PheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGluValMet 872
 DB 1914 TACAAAAGAGGTGATGACCTCCGCAAGATCAGTTTATTCAACGCTTCTTGTGATG 1973
 QY 873 AspAsnIleTyrLysAlaAlaAsnIleAspCysLysLeuAsnProTyrAlaValLeuPro 892
 DB 1974 GACCACCTACTCAATTAGAAAATCTAGATTGACACTTACCTCAACGATCTTGTCA 2033
 QY 893 MetGlyGluMetIleGlyIleIleGluValAlaProAsn-----CysLysThrIle 909
 DB 2034 ACTGACAAAGATGAAGAGATGCTTAATTTATTAGTTCCAGTCTCTTGGACAAATTTCA 2093
 QY 910 PheGluIleGlnValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSer 929

DB 2094 TCAGAAACATCCAGATATTACAAAGTTTACCTACAGAAAGTTCCATCMTGATGAGATGCTCT 2153
 QY 930 PheMetAsnLysTyrPleArgLysGlnCysGlyIleGluAspGluLysLysLysSerLys 949
 DB 2154 TTT-----GGTATTAACGGCTCAATG----- 2174
 QY 950 LysAspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLys 969
 DB 2174 ----- 2174
 QY 970 TyrPheGluSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyr 989
 DB 2175 -----TTGAGACATTTCAAAAAAGCTGCCGCGTTACTCTCATTAACATAC 2222
 QY 990 IleMetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyr 1009
 DB 2223 ATATTGGGGGTTGGAGACAGCATCTGGATATATCTTCTTAACTGATGATGACGCCCTT 2282
 QY 1010 ValHisIleAspPheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArg 1029
 DB 2283 TTTCAATGTGACTTTGCTTTTATCTTGGG-----CGA 2315
 QY 1030 AspArgGlnProPhe-----IleLeuThrGlnHisPheMetThrValIle 1044
 DB 2316 GACCCAAAGCATTTCCGCCACCGATGAGATGTTGTAAAGAA-----ATGGTTGAGGCC 2369
 QY 1045 ArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPheLysThrLeuCys 1064
 DB 2370 ATGGGTGCT-----GCAGAAAGCCAAATATTAACAAAGGTTCAAGTCTTCACTGC 2417
 QY 1065 ValGluAlaTyrGluValMetTyrAsnAsnArgAspLeuPheValSerLeuPheThrLeu 1084
 DB 2418 TGCAGAGATTCACATTTCTAGAGAGTCCAGCATCTCATTTGAATCTTCAAGCTG 2477
 QY 1085 MetLeuGlyMetGluLeuProGluLeuSerThr----- 1095
 DB 2478 ATGGAGCATGACGAGATTCGAGACATCTCTCCGATGAAAGCGAGGCTCAAGCTCAG 2537
 QY 1096 -----LysAlaAspLeuAspHisLeuLysLysThrLeuPheCysAsnGlyGluSer 1112
 DB 2538 GAGAAATTCGCGTTGAGATCTGAC----- 2561
 QY 1113 LysGluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAla 1127
 DB 2562 GACGAGAGGCTATACATTTCTTCCAGGATCTTATCAACGATAGC 2606
 RESULT 8
 US-09-921-330-1
 ; Sequence 1, Application US/09921330
 ; Patent No. US20020102682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Calc, Susan J.
 ; APPLICANT: Wang, Hongyu
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phyate
 ; TITLE OF INVENTION: Metabolism in Plants
 ; FILE REFERENCE: 070603
 ; CURRENT APPLICATION NUMBER: US/09/921,330
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1

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; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (258) ... (2666)
; NAME/KEY: misc feature
; LOCATION: (1) ... (3252)
; OTHER INFORMATION: n = A,T,C or G
US-09-921-330-1

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Alignment Scores:

Pred. No.:	3,71e-54	Length:	3252
Score:	551.50	Matches:	200
Percent Similarity:	38.68%	Conservative:	123
Best Local Similarity:	23.95%	Mismatches:	297
Query Match:	9.12%	Indels:	215
DB:	10	Gaps:	27

US-08-908-453-1 (1-1146) x US-09-921-330-1 (1-3252)

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QY 415 IlegluPheSerValTyValglYThrLeuThrLeuAlaSerLysSerThrThrLysVal 434
DB 381 GTTGAAGTCAGACCTATACATCATGATGGGATCCAAATTGGGCTGCTGTAAACCAAGCTTG 440
QY 435 AenAlaGlnPheAlaLys-----TTPaenLysGluMetTyThrPheAspLeuTyMet 452
DB 441 GAACCTTGTGACCGCAAAATACGTGTGAAT---GACCTCATTAACATTAAGTCAAAATAC 497
QY 453 LysAspMetProProSerLeuAlaValLeuSerLeuArgValLeuTyrgLysValLysLeu 472
DB 498 AAGGACCTTAACATCCCTCTCGACAGCTTGATTAAGGTG-----TGGGATGCTCATCT 551
QY 473 LysSerGluGluPheGluValGlyTTPValAspMetSerLeuThrAspTTPArgSerGlu 492
DB 552 GGTGAACACCTGAGGTTGTCGGTGGAGCCACCATTCTTTTTCACAGCAAAAGGCAG 611
QY 493 LeuArgGlnGlyGlnPheLeuPheHisLeuTTPAlaProGlu----- 506
DB 612 CTTAAACAGAAAGACAGAAAGCTCGCGCTGTGGCCCAACAAAGAGGACGATGAGAGATC 671
QY 507 ProThrAlaAsnArgSerArgLlegLysGluAsnGlyAla----- 519
DB 672 CCACACACAACCTCGTGAAGGTTCTAGGAATGAGAGGGGTGATAGACGTTTGAA 731
QY 520 ----- 520
DB 732 AGGCTTGTAAACAGATGAGAGAGGACAGATACAACTGTGATGGCTTGATGCTCTT 791
QY 522 GlyThrAsnAla----- 525
DB 792 GCCTTAGAGTGTATGACAAAGCTATGCAAAAAGAGTGTGACAGAGGCCAAATTTGTAC 851
QY 526 ---AlaValThrLlegLysSerSerTyrgLysGlyArgValArgMetProSerGlnGly 544
DB 852 CCGAGCTGCTGTTGAATGTGCAAGTTTGCAGAAATGATGCTTCCAGGAATCTGGA 911
QY 545 GlnTyThrTyLeuValLysHisArgSerThrTTPThrGluThrLeuAsnLleMetGly 564
DB 912 GCAAATTTTATACACCGGCCCGACAGTATCATTAACAAATGAATGCTGTACTGTATG--- 968
QY 565 AspAspTyGluSerCysLleArgAspProGlyTyTyLysLysLeuGlnMetLeuValLys 584
DB 969 ---GACCTGAACTTGGAAAGAACCAATCCATCTGACACACAGATTAAGCTTGCTAG 1025
QY 585 LysHisLeuSerGlyLleVal----- 591
DB 1026 AGCTTACCTCGGTGATAGTTGATAGATCTTAAACCAAGCTCAATGAGAGAAGTTA 1085
QY 592 ----- 592
DB 1086 CTACAAACAATATTATTAAGTTCTCTCTACACGACACCTTGAGAGTGTGATGAGAGCAATTG 1145

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QY 600 ValTTPMetTTPArgArgTyrllegLysGlnGluProAspLeuLeuLleValLeuSer 619
DB 1146 GTTGAAGTTTCGTTTCTTTGATGTCAGAGAAAGAGCTTACAGAAATTTGTCCGC 1205
QY 620 GluLeuAlaPheValTTPThrAspArgGluAsnPheSerGluLeuTyValMetLeuGlu 639
DB 1206 TCAGTGAT-----TGGAGTGTATACCAAGAGACGTAAGCAAGCTGTGAGTTGATGGA 1259
QY 640 LysTTPProProSerValAlaAlaAlaLeuThrLeuGlyLysArgCysThrAsp 659
DB 1260 AAGTGGAAATGATGATGTGGCTGATGACCTGATGACCTTCTCTCACTGATTTTGAAGC 1319
QY 660 ArgValLleArgLysPheAlaValGluLysLeuGlnGluLeuSerProValThrPhe 679
DB 1320 GACGAAGTTCTGTGTTATGCTGTACGCTACT---GAAAGGCTGATGAGAAATTA 1376
QY 680 HisLeuPheLleLeuProLeuLleGlnAlaLeuLysTyrgLysProArgLleGlnSerGlu 699
DB 1377 CAGTCTATTATCTCCAGTATGTCAGACCTCTCGCTTGAAGATCTGACAAAGTCCCGT 1436
QY 700 ValGlyMetMetLeuLeuThrArgAlaLeuCysAspTyrgLleGlyHisArgLeuPhe 719
DB 1437 CTAGCACTCTTCTTGTAAACCGTGTGTCACACATGAAATGCTTACGCTTCTCCG 1496
QY 720 TTPLeuLeuArgAlaGluLleAlaArgLeuArgSerCysAspLeuLysSerGluGluTyrg 739
DB 1497 TGGTATATTATTAAGTTGAG-----CTTCACAGTCCGTCATAT 1532
QY 740 ArgArg-----LleSerLeuLeuMetGluAlaTyrgLeuArg----- 751
DB 1533 GCAAGACATATTATGACATATGACATGCTGTGAAAACAGTATGATGAAATTTGTTGCT 1592
QY 752 -----GlyAsnGluGlnHisLleLysLle-----LleThrArgLleValAsp 765
DB 1593 AAGGAGATGGAGATGAAAGATGATTTGACCTGTGGCAGAGTTAACCCGGACAGAC 1652
QY 766 MetValAspGluLeuThrArgLleSerThrLeuValLysGlyMetProLysAspValAla 785
DB 1653 CTCACGTGCTCAATGTGTCTATTATG-----AAGATGTAAAGA 1691
QY 786 ThrMet-----LysLeuArgAspGluLeuArgSerLle 796
DB 1692 AATGTAAAGTAGGACGACAAAGAAATTTGAAATTTAGAGGACCTTATTCACAGAGTT 1751
QY 797 SerHisLysMetGluAsnMetAsp-----SerProLeuAspProValTyrgLys 812
DB 1752 TTCAGTGAAGCTTAACAATTTGATGAGCAATCTGTTACCACTTATGACCAACTTCTTC 1811
QY 813 LeuGlyGluMetLleLleAspLysAlaLleValLeuGlySerAlaLysArgProLeuMet 832
DB 1812 CTAAACAGAGTTGTCTCCCAAGATCGTCTATTTAAGAGTGGCTTGACCTTTGGCG 1871
QY 833 LeuHisTTPProLysAsnLysProLysSerAspLeuHisLeuProPheCysAlaMetLle 852
DB 1872 CTGAATTTTAAACGCAAAATGCGGACATCC-----AAGATTTATTT 1913
QY 853 PheLysAsnGlyAspAspLeuArgLleAspMetLeuValLeuGlnValLeuGluValMet 872
DB 1914 TACAAAGAGGTGATGACCTCGGCAAGATGATGTTGTTATTCACAAAGCTTCTTGATG 1973
QY 873 AspAsnLleTTPLysAlaAlaAsnLleAspCysLysLeuAspProTyrgAlaValLeuPro 892
DB 1974 GACCGACTACTCAATTTAGAAATTTAGATTTGACCTTACTCCATACGAGTTCTTGCA 2033
QY 893 MetGlyGluMetLleGlyLleLlegLysValValProAsn-----CysLysThrLle 909
DB 2034 ACTGACCAAGATGAGAGGATGCTGAATTTTATTAAGTTCAGTTCTCTTGACAGATTTCTA 2093
QY 910 PheGluLleGlnValGlyThrGlyPheMetLeuThrAlaValArgSerLleAspProSer 929
DB 2094 TCAGAACATCGCAGATTTACCAATTCCTACAGAAATTCATCMTGATGAGAGATGCTCT 2153
QY 930 PheMetAsnLysTTPLleArgLysGlnCysGlyLlegLysAspGluLysLysSerLys 949

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Db      2154 TTT-----GGTATAACGGCTCAATGT-----2174
Qy      950 LysAspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLys 969
Db      2174 -----2174
Qy      970 TyrPheGluSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyr 989
Db      2175 -----TTGGAGACATTCATTAAAGCTGGCGGGTACTCTCTCTATTACATAC 2222
Qy      990 IleMetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGlnAspGlyLysTyr 1009
Db      2223 ATATTGGGGGTGGAGACAGCATCTGATATATCTTCTTCACTGATGATGAGCGCTT 2282
Qy      1010 ValHisIleAspPheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArg 1029
Db      2283 TTTCATGTGTGACTTTGCTTTTATCCTTGG-----CGA 2315
Qy      1030 AspArgGlnProPhe-----IleLeuThrGlnHisPheMetThrValIle 1044
Db      2316 GACCCAAAGCCATTTCGCCGACCGATGAAGTTGTGAAGAA-----ATGGTTGAGGCC 2369
Qy      1045 ArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPheLysThrLeuCys 1064
Db      2370 ATGGGTGGT-----GCAGAAAGCCAAATATTACACAAGGTTCAAGTCTACTGC 2417
Qy      1065 ValGluAlaTyrGluValMetThrPheAsnAspArgPheValSerLeuPheThrLeu 1084
Db      2418 TCGGAGACATCAACATCTCTGAGAAAGTCCACAGCTCATTTGATTTCAAGTCT 2477
Qy      1085 MetLeuGlyMetGluLeuProGluLeuSerThr-----1095
Db      2478 ATGGAGCATCGGACATTCGACATCTTCCCGCATGAAGCGAGGCTCAAGTCCAG 2537
Qy      1096 -----LysAlaIleAspLeuAspHisLeuLysLysThrLeuPheCysAsnGlyLys 1112
Db      2538 GAGAAATTCGCGTGTGATCTGCAC-----2561
Qy      1113 LysGluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAla 1127
Db      2562 GACGAGAGGCTATACATTTCTTCCAGATCTTATCAACGATAGC 2606

RESULT 9
US-09-921-329-1
; Sequence 1, Application US/09921329
; Patent No. US2002011084A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; FILE REFERENCE: 0706D2
; CURRENT APPLICATION NUMBER: US/09/921,329
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 09/677,064
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (258) ... (2666)
; NAME/KEY: misc_feature
; LOCATION: (1) ... (3252)
; OTHER INFORMATION: n = A,T,C or G
US-09-921-329-1

Alignment Scores:
Pred. No.: 3,71e-54 Length: 3252
Score: 551.50 Matches: 200
Percent Similarity: 38.68% Conservatve: 123
Best Local Similarity: 23.95% Mismatches: 297
Query Match: 9.12% Indels: 215
DB: 10 Gaps: 27

US-08-908-453-1 (1-1146) x US-09-921-329-1 (1-3252)
Qy      415 IleGluPheSerValTyrValGlyThrLeuThrLeuAlaSerLysSerThrThrLysVal 434
Db      381 GTTAGTCGACGCTATACATGATGATGATCCAAATTTGGGTTGCCGTAAACAAAGCTTG 440
Qy      435 AsnAlaGlnPheAlaLys-----TrpAsnLysGluMetTyrThrPheAspLeuTyrMet 452
Db      441 GAACCTTCTGACCGCAAAATGCTGTGGAT---GAGCTCATACATTAAGTACCAAAATAC 497
Qy      453 LysAspMetProPheSerValValLeuSerIleArgValLeuTyrGlyLysValLysLeu 472
Db      498 AGGAGCTTACATACCTCTCGAGCTTCAATTTACGTTG-----TGGAGTCTCATCT 551
Qy      473 LysSerGluGluPheGluValGlyTyrValAsnMetSerLeuThrAspTrpArgAspGlu 492
Db      552 GGTGAGAACCCGAGGTTGTGTGTGGAGCCACCAATTTCTTTTAAACAGCAAAAGGCG 611
Qy      493 LeuArgGlnGlyGlnPheLeuPheHisLeuThrLapArgLys-----506
Db      612 CTTAAACAGGAGACAGAACCTGGCGCTGGCCACAAAGAGGAGAGATGAGAGAGTC 671
Qy      507 ProThrAlaAsnArgSerArgIleGlyLysGlnGlyAla-----519
Db      672 CCCACCACACTCTCGCAGAGGTTCTTGAATGAGAGGGGTAGATGAAACGTTGGA 731
Qy      520 -----ArgIle 521
Db      732 AGGCTTTTAAAGATAGAGAGGCGACATACACATGTTGATTGGCTTGATGCTGT 791
Qy      522 GlyThrAsnAla-----525
Db      792 GCCTTCAGCTGCTATGACAAAGCTATGAAAAGAGTGTGAGAGAGGCAATTTGTAC 851
Qy      526 ---AlaValThrIleGluIleSerSerTyrGlyArgValArgMetProSerGlnGly 544
Db      852 CTTAGTCTGGTGTGAAATGATGATGCAATCAATCAATATTTCTTCCAGAAATCTGGA 911
Qy      545 GlnTyrThrTyrLeuValLysHisArgSerThrTrpThrGluThrLeuAsnIleMetGly 564
Db      912 GCAATTTTATACACCGGCCAGATATCAATTAATTAAGTGTCAAGATCTGATAG--- 968
Qy      565 AspAspTyrGluSerCysIleArgAspProGlyTyrLysLysLeuGlnMetLeuValLys 584
Db      969 ---GACCTGAACCTTGAAAGAACCAATCATCTGAGCAAGAGCTTAAAGCTTGCTAAG 1025
Qy      585 LysHisGluSerGlyIleVal-----591
Db      1026 AGCTTGACTGCTGGATGTTGATGATAGATCTAAACCAAGCTCAATAGAGAAAGTTA 1085
Qy      592 -----LeuGluGluAspGluGlnArgHis 599
Db      1086 CTACAAACATTAATTAATTTCTCTCTACAGCACCTTGAGAGAGAGAGAGCAATTTG 1145
Qy      600 ValTrpMetTrpArgArgTyrIleGlnLysGlnGluProAspLeuIleValLeuSer 619
Db      1146 GTGTGAGAGTTCGTTCTTCTTGTATGTCTGAGAAAGCTTAAACGAAATTTGTCCGC 1205

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QY 620 GtluuAlaPheValTrrhPargGluAenPheSerGluLeuTyrValMetLeuGlu 639
DB .....
QY 1206 TCAGTGGAT-----TGGAGTGAATACCAAGAACTTAAGCAAGCTTGAATTGATGCA 1259
QY 640 LysTrrPProPProSerValAlaAlaAlaLeuThrLeuGlyLysArgCysThrAsp 659
DB .....
QY 1260 AAGTGGAAATATGATGATGCTGATGACATGACCTTCTCACTGATTTTGAAC 1319
QY 660 ArgValIleArgLysPheAlaValGlyLysLeuSerGluLeuSerProValThrPhe 679
DB .....
QY 1320 GACGAAGTTCGGTATATGCTGACCGTACTT---GAAAGGCTGATGATGAAGAATTA 1376
QY 680 HisLeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGluProArgIleGlnSerGlu 699
DB .....
QY 1377 CAGTGTATTTACTCCAGTTAGTGAAGCTCTTCGGTTGGAAGATCTGACAAAGTCCGT 1436
QY 700 ValGlyMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPhe 719
DB .....
QY 1437 CTAGCACTCTTCTTGTAAACGGTCTTGTCCAAATGCAATGCTGCTTCTCCCG 1496
QY 720 TrrPLeuLysArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGlyTyr 739
DB .....
QY 1497 TGTATATATTAGTTAGT---CTTCACAGTCTCTGCATAT 1532
QY 740 ArgArg-----IleSerLeuMetGluAlaTyrLeuArg----- 751
DB .....
QY 1533 GCAAAGCATATTATGACACATATGACATGCTTGAAGAAACATATGATGCTTGGT 1592
QY 752 -----GlyAsnGluGlnHisIleLysIle-----IleThrArgGlnValAsp 765
DB .....
QY 1593 AGGAGAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1652
QY 766 MetValAspGluLeuThrArgIleSerThrLeuValLysGlyMetProLysAspValAla 785
DB .....
QY 1653 CTCACGTCTCAATGTGTTCTATATG-----AAGATGTGAAGA 1691
QY 786 ThrMet-----LysLeuArgAspGluLeuArgSerIle 796
DB .....
QY 1692 AATGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1751
QY 797 SerHisLysMetGluAsnMetAsp-----SerProLeuAspProValTyrLys 812
DB .....
QY 1752 TTCAGTGAAGCTTAAACAATTTGATGACCAATTCGTTACCAATGACCAACTCTTCTC 1811
QY 813 LeuGlyGluMetIleLeuAspLysAlaIleValLeuGlySerAlaLysArgProLeuMet 832
DB .....
QY 1812 CTAAACGAGATGTGCTCCTCAAGATGCTTATATTAAGAGTGCCTTGAACCTTTGGCC 1871
QY 833 LeuHisTrrPLeuAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIle 852
DB .....
QY 1872 CTGACATTTTAAACACCAATATGCGGACATCC-----AAGATTATT 1913
QY 853 PheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuMet 872
DB .....
QY 1914 TACAAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973
QY 873 AspAsnIleTrrPLeuAlaAlaAsnIleAspCysCysLeuAspProLysAlaValLeuPro 892
DB .....
QY 1974 GACCGCATCTCAATTAATTAAGAAATCTAGATTGACCTTACTCTCAATACGAGTCTTGA 2033
QY 893 MetGlyLysMetIleGlyIleIleGlnValAlaProAsn-----CysLysThrIle 909
DB .....
QY 2034 ACTGGAACAAGATGAAGGATGCTTGAATTTATAGTTCCAGTCTCTTGCACAGATTCTA 2093
QY 910 PheGlnIleGlnValAlaGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSer 929
DB .....
QY 2094 TCAGAACATCGCGATTTTCAAGTACTCAACAGATTCATCATGATGATGATGATGATGAT 2153
QY 930 PheMetAsnLysTrrPLeuArgLysGlnCysGlyIleGlnAspGluLysLysSerLys 949
DB .....
QY 2154 TTT-----GGTATTAACGGCTCAATGT----- 2174
QY 950 LysAspSerThrLysAsnProIleGlnLysLysIleAspAsnThrGlnAlaMetLysLys 969

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DB 2174 ----- 2174
QY 970 TyrPheGlnSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyr 989
DB .....
QY 2175 -----TTGGAGACATTCATTAATAAAGCTGCGGCTTACTCTGATCAATTAACATAC 2222
QY 990 IleMetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGlnAspGlyLysTyr 1009
DB .....
QY 2223 AATTTGGGGTTGGAGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2282
DB .....
QY 2283 TTTCAATGTTGACTTTCCTTATCTTATCTTGG-----CGA 2315
QY 1010 ValHisIleAspPheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArg 1029
DB .....
QY 2316 GACCCAAAGCCATTTCCGCCACCGATGAAGTGTGTGAAGAA-----ATGGTTGAGGCC 2369
DB .....
QY 1045 ArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPheLysThrLeuCys 1064
DB .....
QY 2370 ATGGGTGGT-----GCAGAAAGCCAAATTTTACACAAAGTTCAAGTCTTACTGC 2417
QY 1065 ValGlnAlaTyrGluValMetTrrPAsnAsnArgAspLeuPheValSerLeuPheThrLeu 1084
DB .....
QY 2418 TGGAAAGCATACAAATCTGAGAGAAAGTCCAGAGTTCATTTGAATCTAATCAAGCTG 2477
QY 1085 MetLeuGlyMetGluLeuProGluLeuSerThr----- 1095
DB .....
QY 2478 ATGGAGCATCAGGATTCGCGACATCTCTGCCAGTGAAGCGAGGTCTCAAGCTCAG 2537
QY 1096 -----LysAlaAspLeuAspHisLeuLysLysThrLeuPheCysAsnGlyLysSer 1112
DB .....
QY 2538 GAGAAATTCGGTGTGATCTGAC----- 2561
QY 1113 LysGlnGlnAlaArgLysPhePheAlaGlyIleTyrGlnGlnAla 1127
DB .....
QY 2562 GACGAGAGGCTATACATTTCTTCCAGATCTTATCAACGATAC 2606

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RESULT 10

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US-09-771-161A-10
; Sequence 10, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-10

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Alignment Scores:

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Pred. No.: 2,566-36 Length: 2418
Score: 399.00 Matches: 175
Percent Similarity: 35.59% Conservative: 114
Best Local Similarity: 21.55% Mismatches: 261
Query Match: 6,60% Indels: 262
DB: 10 Gaps: 30

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US-08-908-453-1 (1-1146) x US-09-771-161A-10 (1-2418)


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Db      2136 GAGGAGACATTGACACTTTTGTAGAAATATGACCAAGT----- 2177
Qy      936 ArgLysGlnCysGlyIleGluAspGluLysLysSerLysLysAspSerThrLysAsn 955
Db      2178 -----GAGAAATGGGCCCAAT 2192
Qy      956 ProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyrPheGluSerValAsp 975
Db      2193 GGGATTAGCTGAGGCTC-----ATGGAC 2216
Qy      976 ArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIleMetGlyIleLysAsp 995
Db      2217 ACTTACGTTAAAGCTGCTGCTGATTTGCTGATGACCTATATACTTGAAGTTGAGAC 2276
Qy      996 ArgHisSerAspAsnLeuMetLeuThrGluAspGly 1007
Db      2277 AGGCACCTGATTAACCTTTTGCTTAACAAACAGCA 2312

RESULT 11
US-09-801-368-389
/ Sequence 389, Application US/09801368
/ Patent No. US20020128250A1
/ GENERAL INFORMATION:
/ APPLICANT: Busby, Robert
/ APPLICANT: Cali, Brian
/ APPLICANT: Hecht, Peter
/ APPLICANT: Holtzman, Doug
/ APPLICANT: Madden, Kevin
/ APPLICANT: Maxon, Mary
/ APPLICANT: Milne, Todd
/ APPLICANT: No. US20020128250A1man, Thea
/ APPLICANT: Royer, John
/ APPLICANT: Salama, Sofie
/ APPLICANT: Sherman, Amir
/ APPLICANT: Silva, Jeff
/ APPLICANT: Sumners, Eric
/ TITLE OF INVENTION: Methode for Improving Secondary Metabolite Production in Fungi
/ FILE REFERENCE: 109272.147
/ CURRENT APPLICATION NUMBER: US/09/801,368
/ PRIOR FILING DATE: 2001-03-07
/ PRIOR APPLICATION NUMBER: US 09/487,558
/ PRIOR FILING DATE: 2000-01-19
/ PRIOR APPLICATION NUMBER: US 60/160,587
/ PRIOR FILING DATE: 1999-10-20
/ NUMBER OF SEQ ID NOS: 440
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 389
/ LENGTH: 5703
/ TYPE: DNA
/ ORGANISM: Saccharomyces cerevisiae
US-09-801-368-389

Alignment Scores:
Pred. No.: 6,52e-27 Length: 5703
Score: 325.00 Matches: 151
Percent Similarity: 39.11% Conservative: 120
Best Local Similarity: 21.79% Mismatches: 276
Query Match: 5.38% Indels: 146
DB: 10 Gaps: 29

US-08-908-453-1 (1-1146) x US-09-801-368-389 (1-5703)
Qy      503 TTPAlaProGluProThrAlaAsnArgSerArgIleGluAsnGlnValArgIleGly 522
Db      3829 TGGTTTAAAGACCACTAGCG-----TGGCCATTGGCTCAATAGCTGAATAACAA 3882
Qy      523 ThrAsnAlaValThr-----IleGluIleSerSerTyrGlyArgVal 538
Db      3883 GCAAGATTATCTTTACTAGGACCTTTCTTCACTCACTCAACAAATTAAGCTGCTAAG 3942
Qy      539 ArgMetProSerGlnGlyGlnTyrThrTyrLeu-----ValLys 551
Db      3943 TCACGTCATTGGCGGAAAGATTACAAAGATCTGAACCTATTCTTGGCAAGCAATTCAG 4002

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Qy      552 HisArgSerThrTrp---ThrGluThrLeuAsnIleMetGlyAspAspTyrGluSerCys 570
Db      4003 CAGATTCAACCTGGCTTACTCCGACTGAGAAAGATTGAAGGCGGACCAACAGCAAGCTT 4062
Qy      571 IleArgAspProGluTyrLysLysLeuGlnMetLeuValLysLysGluSerGlyIle 590
Db      4063 ACAAGCGAT-----ATCGTTGAA-----GCT 4083
Qy      591 ValLeuGluAspGluGlnArgHisValTyrMetTyrPheArgGlyTyrIleGlnLysGln 610
Db      4084 ACCTTTGTCTAAAGATCAACATTAGCAATTAATCTTACACAGATGTTATAGCAAGAA 4143
Qy      611 GluProAspLeuLeuIle---ValLeuSerGluLeuAlaPheValTyrThrAspArgGlu 629
Db      4144 GCTGAGAGATGTTTATGAGGCTTACTGTCACAAACGCTTTAATGTGTGTGGGCTCCCA 4203
Qy      630 AsnPheSerGluLeuTyrVal-----MetLeuGluLys----- 640
Db      4204 AGTGTCTTGAACCTGTTCATAAAGAACCACTGACAGATTAAGAAAGACTACAGCA 4263
Qy      641 -----TTPLysProProSerValAlaAlaIleThrLeu---LeuGlyLysArg 656
Db      4264 ACCTTATACCTGGGCGCCGAGTGAGCCGTTAAATCTATCAACCTTTCTCCCAATCG 4323
Qy      657 CysThrAspArgValIleArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerPro 676
Db      4324 CAAGSTAATCTTTTATCTTCAATTCAGCAATATTCGTTGGAATCAACAA-----GAT 4377
Qy      677 ValThrPheHisLeuPheIleLeuPro---LeuIleGlnAlaLeuLysTyrGluProArg 695
Db      4378 GTGAACCTGGCACTTCTTCAATGCTTCTCAATTCGACAAATGTTTATGAGTACAGTAAACC 4437
Qy      696 AlaGlnSerGluValGlyMetMetLeuThrArgAlaLeuCysAspTyrArgIleGly 715
Db      4438 GGATATGTCGAA-----AGATTGATTTGGATCTGCGAATAATTAGTGTATTATTCT 4491
Qy      716 HisArgLeuPheThrLeuLeuArgAlaGluIleAlaArg-----LeuArgAsp 731
Db      4492 CATCAATATATCTGAAATATGCTTCCAAACCTCTCAACAGATGATGAAGTTACAGAA 4551
Qy      732 CysAspLeuLysSerGluGluTyrArgArgIleSerLeuMetGluAlaTyrLeuArg 751
Db      4552 GATGAATCAACCAACCTAGATGCTATTTAGGACGCGATGTTCAAGTTTC----- 4605
Qy      752 GlyAsnGluGlnHisIleLysIleIleThrArgGlnValAspMetValAspGluLeuThr 771
Db      4606 ---AGCCAACTCATCGCGATTTTACGAACTGAATTGAAATTTCTTCGACGCAAGTAAT 4662
Qy      772 ArgIleSerThrLeuValIleGlyMetProLysAspValAlaThrMetLysLeuArgAsp 791
Db      4663 GGCATATCTGTTAAGTAAACCATACATTAATAAAGTAAGCTGAAG----- 4713
Qy      792 GluLeuArgSerIleSerHisLysMetGluAsnMetAspSerProLeuAsp----- 808
Db      4714 -----AAACATTAAGATCATGAAGAAATGCAAAATAGAGTGAACCT 4758
Qy      809 -----ProValTyrLysLeuGlyGluMetIle---IleAspLysAlaIle--- 822
Db      4759 GATGTTATTATTCCTTCAATCTGACGCTGATGATTGATTAATGATCGAAGAGTGT 4818
Qy      823 -----ValLeuGlySerLysAlaLysArgProLeuMetLeuHisTyrLysAsnLysAsnPro 840
Db      4819 AAGCCACTTCAATCTCACGCAAGGCGCTTTATAGGCACTTTAAATTAAGAAAGAC 4878
Qy      841 LysSerAspLeuHisLeuProPheCys-----Ala 850
Db      4879 GTTAAAGAT-----CTTTGACAGGTAAACAAAGAACTGAATAATGCAAGCT 4929
Qy      851 MetIlePheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGlu 870
Db      4930 GCTATCTTCAAAAGTGGTGATGATCTGTAGGCAAGATGTTTACGCGTTCAATTAATTCG 4989

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Qy 871 ValMetAspAsnIleThrLysAlaIleAsnIleAspCysCysLeuAsnProTyrAlaVal 890
Db 4990 CTATTAGAACCACTTGGTCTAGTATGCGCTGAGATGCTAGCTTTTCCCTACAGAGTT 5049
Qy 891 LeuProMetGlyGluMetIleGlyIleIleGluValProAsnCysLysThrIlePhe 910
Db 5050 ACTGGACGGCAGCCGGTGTGTCATCGATGATGCTCCCAAT-----TCGGATATCC 5103
Qy 911 GluIleGluValIleThrGlyPheMetAsnThrAlaValAspSerIleAspProSerPhe 930
Db 5104 CGTGAATGTTAGG-----CGTGAAGCTGTAATGATGATGATGATGATTTTC 5151
Qy 931 MetAsnLysTrpIleArgLysGlnCysGlyIleGluAspGluLysLysSerLysLys 950
Db 5152 ACTAGTAATTT----- 5163
Qy 951 AspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyr 970
Db 5164 -----GGTAACTGAATCTACTATCGAATTT 5187
Qy 971 PheGluSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIle 990
Db 5188 CAATAACGCGACCAACCTTGTAAATCTTAGCGGGATATAGCGTAATTTTCGATTTTG 5247
Qy 991 MetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrVal 1010
Db 5248 TTGCAATTCAGAGATAGCATATATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 5307
Qy 1011 HisIleAspPheGlyHisIleLeu-----GlyHisGlyLysThrLysLeuGly 1026
Db 5308 CATATCGATTTGGGTTTATTTTGTATTTGATTTGTCACAGGT-----GGT 5349
Qy 1027 IleGluAspArgGlnProPheIleLeuThrGlnHisPheMetThrValIleArgSer 1046
Db 5350 ATCAAGTTTGAACGATACCTTCAAGCTGACGAGAAATGATGATTAAGTATG----- 5403
Qy 1047 GlyLysSerValAspGlyAsnSerHisGluLeuGln-----LysPheLysThrLeu 1063
Db 5404 -----GGAGGTTCCGCCACGACCCACGCGCTATCTGAGACTTGAAGAACTT 5448
Qy 1064 CysValGluAlaIleTyrGluValMetTyrAsnAsnArgAspLeuPheValSerLeuPheThr 1083
Db 5449 TGTATCAAGGCGATATCTAGCCGCCGTCGACGTCGAGCCATATATGATGTTGAAT 5508
Qy 1084 LeuMetLeuGluMetGluLeuProGluLeuSerThrLysAlaAspLeuAspHisLeuLys 1103
Db 5509 CCTATGTTAGGAAGCGGTCTCCCTGCTTAAAGGTCACAGACATTTAGGAATCTAAGA 5568
Qy 1104 LysThrLeuPheCysAsnGlyLysLeuSerLysGluGluAla----- 1116
Db 5569 GCAAGATTTCACACCTCAAAAACCGATCGAAGCTGCACTATATATGAGCGCTAATC 5628
Qy 1117 ArgLysPhePheAlaGlyIleTyrGluGluAlaPheAsn 1129
Db 5629 CGTAAAGTTATGAAGTATATTCATTAAGGTTATGAT 5667

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; LENGTH: 2620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (1838)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (2596)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (2609)
; OTHER INFORMATION: n equals a,t,c,g, or c
US-09-925-302-205

Alignment Scores:
Pred. No.: 1.34e-25 Length: 2620
Score: 309.00 Matches: 230
Percent Similarity: 33.46% Conservative: 134
Best Local Similarity: 21.14% Mismatches: 374
Query Match: 5.11% Indels: 351
DB: 10 Gaps: 46

US-08-908-453-1 (1-1146) x US-09-925-302-205 (1-2620)

Qy 129 PheProMetLeuPheLeuTyrGlnProAsp---GlyIleAsnArgAspLysGluLeuMet 147
Db 39 TTCAGAGTAATGTTCTGCTACTTGAAGATTAAGCTAATTCAGAAACAAA----- 89
Qy 148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGlnGluSerLeu----- 165
Db 90 TCTGGAGATGATCAGATGTGTGATTCAGTCCGCGCAAAAGTATTCGATCTCTCTGAAC 149
Qy 166 -----AspGluGluLeuArgGlnPheArgAla 174
Db 150 ATGATGCGCGATTAAGCCAGACCAAGACAGAGAGAGAGAGCTGAGCGGACGTCAGT 209
Qy 175 SerLeuTyrPalaArgThrLysLysThrCysLeuThrArgGlyLeuGlnGly-----Thr 192
Db 210 TCTGTTGGTGAATCTCA-----ACCACATCCACAAAGAGATTAAGAGGTTGCGACAGCA 263
Qy 193 SerHisTyr-----AlaPheProGluGlnGlnTyrLeuCysValGly-Gl 207
Db 264 AGTATCTATCTGCTGCTGCTGATAGTATTTCCC-----ACTTGCTCTGAGAGCG 311
Qy 207 userCysProLysAsp-LeuGluSerLysValLysAlaIleLysLeuSerTyrGlnMetP 227
Db 312 GGACTGTGCTGAAGCCATGCTGAGACATCTGACACACCTGTCACCTGTCTCTG----- 364
Qy 227 heTPrArgLysArgLysAlaGluIleAsnGlyValCysGluLysMetMetLysIleGlnI 247
Db 365 -----AGCCTGATATTCAC-----AAGATATCAC 389
Qy 247 IleGluPheAsnProAsnGluThrProLysSerLeuLeuHisThrPheLeuTyrGluMetA 267
Db 390 CTACTATGACATCCCGACCGCCCTACCGGATACGGTTCTCTGACACGTAAGAGCCG 449
Qy 267 rGlyLeuAspValTyrAspThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuA 287
Db 450 GTGAAGACATTTGT-----AAGACTTCGCTGACAGCGCTGGAGATGATCTCTCCAGAG 503
Qy 287 IagLysArgThrThrPheValThrAsnProAspValLysLeuThrSerTyrAspGlyValA 307
Db 504 CCATGAAGTGGCA-----CTACCGCTC-----ACCA 530
Qy 307 rGSerGluLeuGluSerTyr-----ArgC 315
Db 531 AGTCCACCTCGAGAAATATCTGAACAACATNAGACTGGGTATCGGAGCTGCCAGC 590
Qy 315 yEPProGlyPheValAlaArgArgGlnSerLeuValLeuLysAspTyrCysArgProLysP 335

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Db 591 AACAGGGGCTGGCCATGGCCACTGAGACATCCTT----- 625
 Qy 335 roleuylglubProhiSTyrgValArgAlahieglubrglyleuAlaleuAspValleus 355
 Db 626 -----CACTTGTGCTGAGTCAACAGACAGAACCAACTTGTGGGCAACTC 671
 Qy 355 eValSerlleasPserThrProlysglnSerlysaSnsPserMetValmetThrAsp 375
 Db 672 ACCTGAGC-----G 680
 Qy 375 hArgPProThraLaseleuLyglnValSerleuTriPasleuAspAlaAsnleuMet 395
 Db 681 AGCGCGCGGCTGTGAGAGAAAGACTACTCCAACTTCATGGATCCCGATCTCGCGA 740
 Qy 395 lArgProValAsnleuSerGlyPheAspPheProAlaAspMetTyrgValArg 415
 Db 741 ACCGCTACCGGGGCT-----GAGGTGATGCAATGA 770
 Qy 415 lglubPheSerValTyrgValGlyThreuthleuAlaSerlySserThrThrlyS--V 434
 Db 771 TTCGTTCTTCAGGACACACAGAGATGTGACTGAAACAATGATGTCCAGGATC 830
 Qy 434 aAlaAsnlaGlubPheAlaTySTPasnlysglnMetTyThrPheAspleuTyrg 451
 Db 831 TACATTCACCTTACGCCAGATCCTCAGACATCACAGCGCATCTTCACACTGA 890
 Qy 452 -----MetlyAspMetProProSerAlaValleuSerlleArgVal 466
 Db 891 CCGCAATGCTCATTAAGCAATTAAGATTGACCCG----- 925
 Qy 466 eutyrollylyvallylyleuLysercluglnPhegluValGlyTTPValaAsnMetSer 486
 Db 925 ----- 925
 Qy 486 euthraSPTrpArgAspGlnleuArgGlnGlylnPheleuPhehileu---TTPAlaP 505
 Db 926 -----CAGTCTCTTCACTCATCTGTGCTGGGGTC 953
 Qy 505 roglubProThraLaaAsnArgserArglleGlyglubnglyAlaArglleGlyThraAsn 525
 Db 954 CCGT--CCGATGTTCATGACGATGACATGACAGACCCCTGCTGGAGTGGCTG 1012
 Qy 525 lAlaValaThrillegluileSerSerTyrglyArgValArgMetProserGlnGly 545
 Db 1013 CTGGC-----TGGCAAGATGAGTGAAGTGC--GTTCTCGGT----- 1050
 Qy 545 lntyThrTyrgleuVallylyshAsArgserThrTrpThrglnuthleuAsnleuMetGlyA 565
 Db 1051 -----CACCTGGGACACACATCGA----- 1068
 Qy 565 sPAspTyrgluSerCyylleArgAspProGlyTyrglylylyleuGlnMetleuVallyl 585
 Db 1069 -----CGCCGATC----- 1077
 Qy 585 yshiegluSerGlylleValleuGlnGlnAspGlnGlnArgHisValITPmetTrpArg 605
 Db 1078 -----TCAGAGCTCAGCCATGTGCTGTGCTG-- 1104
 Qy 605 rGlyTlleGlnlysglnGlnProAspPheleuIleValleuSerGlnleuAlaPheVal 625
 Db 1105 -----GCGGCCACGAGCYCACCC----- 1122
 Qy 625 rPThraPArgGlnAsnPheSerGlnleuTyrgValleuGlnGlySTTPlyAsPProPro 645
 Db 1123 --ACAGGCTCTCTCTCTCTCAGCATGAC-----CCGCGCG 1159
 Qy 645 eValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 665
 Db 1160 ACCCTCTCACGGGCT-----CAGTACGGGGTGAAGTCTCTCGGCTCT 1201
 Qy 665 heAlaValaGlnlylyleuAsnGlnGlnleuSerProValThrPhehileuPheleuP 685

Db 1202 TC-----CCTCGGACGCCCATCTCTTMTACATCCCC 1234
 Qy 685 roleuIleGlnAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 705
 Db 1235 AGATTGTACAGCCCTCAGTACAGC-----AAGATGGCTATGTGGAGATATATTC 1288
 Qy 705 euthraAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 725
 Db 1288 TGTGGGACGCTTAATCCACAGCTTCTGGCACACCATTCATCTGAAACATGAAGACTA 1348
 Qy 725 lulle-----AlaArgleuArgAspCyAspPheleuLyserGlnGlyTyrg 740
 Db 1349 ACATTATTCATGATGAAGAGGCCACAGAAAGCCCTGACATCGCGCAC----- 1398
 Qy 740 rGArglleSerleuMetGln-----AlaTyrgleuArgGlyyAsnGlnGlnHis 757
 Db 1399 --CTCTGATCAGTGTGTGAGAGAGATCACAGGCTCTGTGCGGCCAGCGAAG-- 1452
 Qy 757 lelyllellethraGlnValaAspMetValaAspGlnleuThraArglleSerThre 777
 Db 1453 --GACTTTTACAGCGGAGATTGATTTCTTAAACAATCACCAAGTGTGCTATCA 1510
 Qy 777 alysglyMetProlysaAspValaAlaThrMetlylyleuArgAspGlnleuArgSer 795
 Db 1511 TCAAGCCCTACCTTAAGC-----GACGAGAGAAAGAGGCTT 1549
 Qy 796 --lleSerHileuMetGlnAsnMetAspSerPro----- 806
 Db 1550 GTCTGTGCGCCCTGTCTGAAGTGAAGTGCAGCCGCTGCTCTGCTCCAGCAACCTG 1609
 Qy 807 -----leuAspProValTyrglylylyleuGly 814
 Db 1610 AGCCATTGTGTGAACRTCACTCACTCAAGTCTGGACCCCATGAGAGTGTGCAAAAG 1669
 Qy 815 -----GluMetllelleAspAlaAla 822
 Db 1670 CCCCATATCTGCGCAAGTTCAAGTGAAGCATGTGAGTTGATGAACCTTGAAGAAAG 1729
 Qy 823 ValleuGlySerAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 842
 Db 1730 GTCTCGGCGCGCTCAGCTCAGAGTGAAGTGAAGCAGCAGAGAGGCCAGCGCAGAA 1789
 Qy 843 AspleuHileuProPheCy--AlaMetllePheLyAsnGlyyAspAspPheleuArg 862
 Db 1790 GATCTC-----CTGGCAGGACGACATCTTCAAGTGGAGAGAGAGCTGCGGAGANA 1840
 Qy 862 PheleuValleuGlnValleuGlnValaMetAspAsnleuTyrglyAlaAlaAlaAla 882
 Db 1841 CATGCTGGCGCTGACAGATCATGACCTCTTCAAGAACATCTTCCAGCTGTGCGGCTGGA 1900
 Qy 882 PCySerCySleuAsnProTyrgAlaAlaValleuProMetGlyGluMetlleGlylle 902
 Db 1901 CCTCTTTGTTTTCCTTACCGGTGTGCGCACTGCCCTGGGTGGGTGATGAGAGT 1960
 Qy 902 lValProAsnCylySThrillePheGlnlleGlnValaGlyThrglyPheMetAsnThra 922
 Db 1961 CATCCCACTCAGCTCCCGGACACAGTGGCCGCGCAGACAGACTT----- 2009
 Qy 922 aValArgSerlleAspProSerPheMetAsnlySTPilleArglyGlnCyGlylle 942
 Db 2010 -----GCGATGACACTACTTACACCCCGGATGACGG-- 2042
 Qy 942 lAspGlnlylylyserlylyleuAspSerThrlysaPProlleGlnlylylyleu 962
 Db 2043 -GATGATCCACCTGCGCTTCCAGAGGCCCGCTACAC----- 2081
 Qy 962 pAsnThrglnAlaMetlylySTyrPheGlnSerValaAspArgPheleuTyrgCy 982
 Db 2082 -----TTCATCCGAGCATGCG 2098
 Qy 982 lglTyrgSerValaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 1002
 Db 2099 CGCTTACAGCTCTCCTGTCTGTCTGTGATCAAGAGCAGACACAGCAACATTAAT 2158

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Oy      1002 LeuThGlnuBpGlyysrYrValHsiLeaBpPheGlyHsiLeleuGlyHsiGlyly 1022
Db      2159 GCTGACACAAAGGGYCATATCATCCATCCATCGACTTTGGCTTCATGTTT-----GA 2209
Oy      1022 sThLyLeuGlylYlleglnHrGAspAsglnPrOpheHleleuThGlnHsiBpHeWTh 1042
Db      2210 AAGCTCCCGGGCGGCAATCTCGGCTGGGAACCCGACATCAAGCTGACGGATGAATGCT 2269
Oy      1042 rValHleArSerglYlysserValaBpGlyAaBserHsiGluLeuGlnlyBpHeLysth 1062
Db      2270 GATATATCATGGGGGGCAAGATG-----GAGGCCACACCTTCAGAGTGTTCATGGA 2320
Oy      1062 rLeuCyValGlnuAlaTyrGluValMetTrpAaAaBpAspLeuPheValSerleuph 1082
Db      2321 GATGTGTGTCCGAGGACTTACCTGGCTGTGGCGCCCTACATGAGACGGGTGTCTTCCTGT 2380
Oy      1082 eThrLeuMetleuGlyMetGluLeuProGluLeuSerThrLyValaAspLeuAspHsiLe 1102
Db      2381 CACTCTCATGTGTGGACACGGGCTCGCC-----TGTTTTCGGGGCAGACATCAAGCT 2434
Oy      1102 uLyValeThrleuBpHeCyAsanGlyGluSerLySGluGlnuAlaArgLyBpHeAlaGt 1122
Db      2435 CTTGACACACAGGTTTAGCCCCCAACATGACTGAGCGGAGGCTGCAAATTTCATCATGAA 2494
Oy      1122 yLleTyrGluGlnuAla 1127
Db      2495 GGTCAATCCAGAACT 2510

RESULT 13
US-09-834-975-805
; Sequence 805, Application us/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffle, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: OF THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF HUMAN CANCERS
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 805
; LENGTH: 7864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(7864)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-805

Alignment Scores:
Pred. No.:      4.18e-21      Length:      7864
Score:          278.00      Matches:      133
Percent Similarity: 40.20%      Conservative: 107
Best Local Similarity: 22.28%      Mismatches: 236
Query Match:     4.60%      Indels:     123
DB:             10      Gaps:       24

US-08-908-453-1 (1-1146) x US-09-834-975-805 (1-7864)
Oy      595 AspGluGlnHrGHisValTrpMetTrpArgArgTyrIlleglnLySGln-----GluPro 612
Db      1280 AACGAAACAGCGACGAAACCCCTAAAGTGGAGAAATAGATAGATAGAGAGCTCTCCTCCAGACACGG 1339
Oy      613 AspleuLeuIleValLeuSerGluLeuAlaPheValTrpThraAspArgGluAnBpSer 632

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Db	1340	AGAGATTGAAATATTCATTCAAGTTCCCTGTTCCAGCTGGCTCCGAGAGAAATTCATCA	1399
Qy	653	GlueuYrYalMetLeuGlulYleTrpIysProSerValAlaAlaLeuThrLeu	652
Db	1400	AGT-----CCCTGATGGGATCGGCAAGCGG-CTGGCCACCTCCCGACC	1443
Qy	653	LeuGlYlsAArgCySThrAspArgValIleArgYsPheAlaValGlulYleuAnslu	672
Db	1444	AAAGAGCAGAAA---ACACAGAGGCTGATTCACAGCTCTCCGG-----CTCAACCAT	1494
Qy	673	GlueuY-----SerProValThrPheAlaPheLeu	684
Db	1495	AAAGTCCCTGGCCGAGTCTGGCTGCCACTGCTGGCTTTGACACACAGTGGTCCGTTGA	1555
Qy	685	ProleuIleGlnAla-LeuYsTYrGlulProArgAlaGln-----	697
Db	1555	CCCCACACACAGGCTGTGTCTCCTCAACTCCAAAGACAAAGGCTCCCTACCTGATTTATGTG	1614
Qy	698	-SerGlulValIleMetLeuLeuThrArgAlaLeuCyAspYrArgIleGlyIleAtr	717
Db	1615	GAAGTCTCTGTATGTGAAACTTTGACACCAACAGTGC-CTTGCCCGAGATCCCGAGAA	1673
Qy	717	gIeuPheTrpLeuYrLeuArgIaGluIleAlaArgLeuAArgPyrCyAspLeuYsSerGI	737
Db	1674	CCGAATTCCGAGTACAGAGTCC---GTGAAAACTTGCCGAAATGTGTTATTCACATGA	1730
Qy	737	uGlulYrArgArgIleSerLeuLeuMetGluAlaTYrLeuArgIleAnslu-----	754
Db	1731	GCACGAGCTGGCAGCTTCACAGCTGTGCCAACTATACAAAGATGATGAGCGCTGTG	1790
Qy	755	-----GlnHisIleLeuIleIleThrArgIlnValAs	765
Db	1791	GATGGATGACATAGGCGAGCTGCAAGTGAAGCTCCCGAATGTGATTCACCAACAGCTGTGA	1850
Qy	765	pMeValAspIuLeuThrArgIleSerThrLeuValYsEluMetProYlsAspValAl	785
Db	1851	CMACTCTCCCAAGTTCTCT--GTGACAGCATACACGACGAGAGCAAGAGAGAGCTGT	1907
Qy	785	aThrMetYsLeuArgAspGluLeuArgSerIleSerHisYsLeuGluAsnMetAspSe	805
Db	1908	GTTGATTTCGACAGGAGGACATCCCGCGGCTTTCCGAACAGCTGCTATACCCGAC	1966
Qy	805	r-----ProleuAspProValTYrYleuGlulMetIleIleAspYl	820
Db	1968	AGCCTTCACAAAGAACCCAGAAAGATCTT-----TC	1997
Qy	820	AlaIleValIleuGlYserAlaYsArgProleuMetLeuHisTrpYsAnsluYs----	838
Db	1998	TGCAGTTCCTC-----AAAGAGCC--TCGCGAGGAAAGATACG	2036
Qy	839	-----AspProYsSerAspLeuHisIleuPro-----PheYsAl	850
Db	2037	GGCGATCAGAGAGGCTCCCTCCCTACGGC-----CATCTCCCAATTGGCGGCTCTGT	2099
Qy	850	ameIlePheYlsAnsluYsAspLeuArgGlnAspMetLeuValIleuGlnValIleuGl	870
Db	2091	AGTCATTGTCAAGTGTGGGATGACCTTCGSCAAAGAGCTTCTGGCGCTTTCAGAGTTCGA	2150
Qy	870	uValMetAspAsnIleTrpYsAlaAlaAsnIleAspCySeYsLeuAsnProTYrAlaVa	890
Db	2151	GCAACTGAGTCCATTGGGAAACAGAGCGAGTCCCTTTGGATGACAGCATACAGAT	2210
Qy	890	IleuProMetGlYgluMetIleGlyIleIleGluValIValProAnsluYsTrpIlePh	910
Db	2211	TCTTGTGATTTCCGCTGATGACTGCAATTTGAACCAAGTGTCAATGCTGTCTCATCA	2270
Qy	910	egluIleGlnValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPh	930
Db	2271	TCAGGTG-----	2277
Qy	930	eMetAsnYsTrpIleArgYlsGlnCyseGlyIleGluAspGluYlsYlsYsSerYlsYl	950

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Db      2278 -----AGAAACAGTCACAGCT 2294
Qy      950 sAspSerThrIysAsnProIleGluLysIleAspAsnThrGlnAlaMetLysLysTy 970
Db      2295 CTCCTTGCTCGATTCTTCTACAGAG-----CACGCGACTTCACCACTCAGGCAATT 2348
Qy      970 rPheGluSerValAspArgPheLeuTySerCysValGlyTySerValAlaThrTyr11 990
Db      2349 CCTCAGTCACAGCCGCAATTGTGCAAGTTGTGCTGGTGTCTGCTGCTGCTTCTTCTACT 2408
Qy      990 eMetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGlnAspGlyLysTyrVa 1010
Db      2409 GCTGCAGTCACAGCAGCAGCAGATGCGATATCTTTGGACGCGAAGGCGCATCATCT 2468
Qy      1010 HisIleAspPheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArg 1030
Db      2469 CCACATCGCACTTGGCTTCTCTCTCCAGCTCACCCGCAAACTCTGGGCTTT-----GA 2522
Qy      1030 pArgGlnProPheIleLeuThrGlnHisPheMetThrValIleArgSerGlyLysSerVa 1050
Db      2523 GAGTCGACGCTTTAAGCTACACACAGAGTTTGTGATGTGATG-----GGCGGCGCT 2573
Qy      1050 LAspGlyAsnSerHisGluLeuGlnLysPheLysThrLeuCysValGlnAlaTyrGlnVa 1070
Db      2574 GGATGCGGCAATG-----TTCACTACTATAAGATCGTGAATGCGTCAAGGCGTATTGC 2627
Qy      1070 LMetTrpAsnAsnArgAspLeuPheValSerLeuPheThrLeuMet--LeuGlyMetG1 1089
Db      2628 CCCTCGGAACAACATGACACAGAGTGTGCGAGATCGGAGATCATCTACAGCAAGTTCTCA 2687
Qy      1089 uLeuProGluLeuSerThrLysAlaAspLeuAspHisIleLysLysThrLeuPheCysAs 1109
Db      2688 GCTCTCTCTCTCTTCATGCTGCTCCAGCACCATTCGAAACCTCAAGAGAGAG--TTCCACAT 2744
Qy      1109 nGlyIleuSerLysGluGlnAlaArgLysPhePheAlaGlyIleTyrGluGlnAlaPheAs 1129
Db      2745 GAGCATGATGAGAGGACAGCTGACGCTG-----CTGCTGACACAGATGTGTGA 2792
Qy      1129 nGlySerThrPheThrLysThrAsnTrpLeuPheHisAlaValLysHis 1145
Db      2793 TGGCAGTATGCGGTCTATCATCCACCAAACTATGACGCGCTTCAGTAC 2841

RESULT 14
US-09-976-165-29
; Sequence 29, Application US/09976165
; Patent No. US20020107383A1
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASANO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONUGATING ENZYME
; FILE REFERENCE: Q-53599
; CURRENT APPLICATION NUMBER: US/09/976,165
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/565,538
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 2451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-165-29

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Alignment Scores:
Pred. No.: 1,5e-19 Length: 2451
Score: 257.50 Matches: 131
Percent Similarity: 39.87% Conservative: 107
Best Local Similarity: 21.94% Mismatches: 239
Query Match: 4.26% Indels: 122
DB: 10 Gaps: 26

US-08-908-453-1 (1-1146) x US-09-976-165-29 (1-2451)
Qy      595 AspGluGlnArgHisValTrpMetTrpArgArgTyrIleGlnLysGln-----GluPro 612
Db      869 AACGAAACGCCAGCAACCTTAAGTGAAGATGAGATGAGAGAGCTCTCTCCAGCACCG 928
Qy      613 AspLeuLeuIleValLeuSerGluLeuAlaPheValTrpThrAspArgGluAsnPheSer 632
Db      929 AGAGTATGATTAATTCATTCACTTCCCTGCTTCCAGCTGCTCTCCAGAGAAATTCATCA 988
Qy      633 GluLeuTyrValMetLeuGluLysTyrLysProPheSerValAlaAlaIleuThrLeu 652
Db      989 AGT-----CCCTGATGCGGATCGGACCGG-CTGGCCAGCTCCCCACC 1032
Qy      653 LeuGlyLysArgCysThrAspArgValIleArgLysPheAlaValGlnLysLeuAnglu 672
Db      1033 AAAGAGCAGAAA--ACAAGAGGCTGATCTCAGAGCTCTCCCTG-----CTCAACCAT 1083
Qy      673 GlnLeu-----SerProValThrPheHisLeuPheIleLeu 684
Db      1084 AAGCTCCCTGCCGAGTGTGCTGCCACTGTGCTTTGACACACAGCTGTGCTGTGA 1143
Qy      685 ProLeuIleGlnAla-LeuLysTyrGluProArgAlaGln----- 697
Db      1144 CCCACACACAGGCTGTTGTCTCTCACTCCAGACGAAAGGCTCCTACTGATTATGTG 1203
Qy      698 -SerGluValGlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisAr 717
Db      1204 GAAGTCCTTAATGTAAGAACTTTGACACACACAGCTTC--CTGCCGAGATCCCGAGAA 1262
Qy      717 GluPheThrPheLeuAlaGlnIleAlaArgLeuArgAspCysAspLeuLysSerG1 737
Db      1263 CCGAATTCGAGATGACAGATCC--GTAGAAAACCTGGCCGAATGTGATTATCCCATGA 1319
Qy      737 uGluTyrArgArgIleSerLeuLeuMetGlnAlaTyrLeuArgGlyAsnGlu----- 754
Db      1320 GCAGCAGCTGCGACCTTCAGCATCTGTGCCCACTATGACAAAGATGAGCGCTGTGC 1379
Qy      755 -----GluHisIleLysIleIleThrArgGlnValAs 765
Db      1380 GGTGATGACATAGGCGAGCTGCAAGTGAAGTCCCGCAAGTCATGACACAGCTGTGA 1439
Qy      765 PheValAspGluLeuThrArgIleSerThrLeuValLysGlyMetProLysAspValAl 785
Db      1440 CAACATCTCCCACTTCTCT--GTGACAGCATCCACGCGAGAGAGAGAGAGAGCTGT 1496
Qy      785 ThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsnMetAspSe 805
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Qy      805 r-----ProLeuAspProValTyrLysLeuGlyGluMetIleIleAspLys 820
Db      1557 ACCTTCAAAAGAGACCCAGAGATCT-----TC 1586
Qy      820 AlaIleValLeuGlySerAlaLysArgProLeuMetLeuHisTyrLysAsnLys----- 838
Db      1587 TCGAGTGTCTTC-----AAAGAGCC-----TGCAGAGAAAGTACG 1625
Qy      839 -----AsnProLysSerAspLeuHisLeuPro-----PheCysAl 850
Db      1626 GCGGATCAGAGAGGCTCCCTTACGGC-----CATCTCCCAATGGCGGCTCTGTGC 1679
Qy      850 AsnIlePheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuG1 870
Db      1680 AGTCATTTCAGAGTGTGGGATGACCTTCGCGCAAGGCTTCTGCGCTTCAGGTGTGA 1739

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QY 805 r-----ProLeuaspProValTyrIysLeuGlyGluMetIleIleAspIy 820
Db 1593 AGCCTTCAACGAGACCCAGAGATCT-----TC 1622
QY 820 sAlaIleValleuGlySerAlaIysArgProLeuMetLeuHisTyrPlyAsnIys----- 838
Db 1623 TGCAGTGTGCTC-----AAAGAGCC-----TGCACGAGAGAAAGTACG 1661
QY 839 -----AsnProIysSerAspLeuHisLeuPro-----PheCysAl 850
Db 1662 GCGGATCAGAGAGGCTCCCTACGCGC-----CATCTCCCAATTGGCGGCTCTCTGC 1715
QY 850 aMetIlePheIysAsnGlyAspAspLeuArgGlnAspMetLeuValleuGlnValleuG 870
Db 1716 AGTCATTGTCAAGTGTGGGATGACCTTGGCAGAGAGCTTCTGGCCTTCAAGTGTGCA 1775
QY 870 vValMetAspAsnIleTyrAlaAlaAsnIleAspCysCysLeuAsnProTyrAlaVa 890
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Db 1891 -----TCCATCCATCAGGTGAAGAAACAGTCACAGCT 1922
QY 950 sAspSerThrIysAsnProIleGluIysIysIleAspAsnThrGlnAlaMetIysIysTy 970
Db 1923 CTCCTTGCTCGATTACTCTCTACAGAG-----CAAGCAGTTACCAACCACTGAGGCATT 1976
QY 970 rPheGlnSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrI 990
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Db 2037 GCTGCAAGTCAAGACAGACAGACATGGAATATCTTTGAGACGACAAAGCCACATCAT 2096
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QY 1050 lAspGlyAsnSerHisGluLeuGlnIysPheIysThrLeuCysValGlnAlaTyrGluVa 1070
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QY 1070 lMetTyrAsnAsnArgAspLeuPheValSerLeuPheThrLeuMet---LeuGlyMetG 1089
Db 2256 CGCTCGAAGAACATGACAGAGTGTGAGATCGTGAATCATCAGCAAGCAAGTTCTCA 2315
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Db 2373 GAGCATGACTGAGAGACAGCTGCAGCTG-----CTGTGAGAGCAGATGTGTGA 2420
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Db 2421 TGGCAGTATGCGGCTTATACCAACAACTTATGACGGCTTCCAGTAC 2469
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Job time : 989 secs

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2003, 01:40:09 ; Search time 191 Seconds
(without alignments)
5626.154 Million cell updates/sec

Title: US-08-908-453-2
Perfect score: 3504
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3504	100.0	3504	4	US-08-857-076-47
2	146.4	4.2	3207	1	US-08-162-081B-35
3	146.4	4.2	3207	2	US-08-780-872-35
4	146.4	4.2	3207	4	US-09-085-957-35
5	130	3.7	3240	1	US-08-162-081B-34
6	130	3.7	3240	2	US-08-780-872-34
7	130	3.7	3240	4	US-09-085-957-34
8	130	3.7	3412	1	US-08-162-081B-32
9	130	3.7	3412	4	US-08-780-872-32
10	130	3.7	3412	4	US-09-085-957-32
11	103.6	3.0	5220	3	US-09-357-070-1
12	103.6	3.0	5220	2	US-08-777-405A-1
13	103.6	3.0	5220	2	US-08-977-871A-1
14	103.6	3.0	5220	2	US-09-225-951-1
15	96.4	2.8	3808	2	US-08-916-917-3
16	96.4	2.8	3808	2	US-08-972-631-3
17	96.4	2.8	3808	2	US-08-972-633-3
18	96.4	2.8	3808	2	US-08-972-630-3
19	96.4	2.8	3808	2	US-08-672-211-3
20	96.4	2.8	3808	2	US-09-225-170-3
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22	90	2.6	5162	2	US-08-916-917-13
23	90	2.6	5162	3	US-09-225-170-13
24	86.8	2.5	4134	2	US-08-817-090B-1
25	86.8	2.5	4137	2	US-08-817-090B-1
26	68.6	2.0	5061	4	US-09-355-160D-1
27	65.6	1.9	5285	2	US-08-609-049A-29

28	55.4	1.9	5285	4	US-09-170-996-29	Sequence 29, Appl	
29	65.6	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl	
30	49.8	1.4	6831	2	US-08-609-049A-27	Sequence 27, Appl	
31	49.8	1.4	6831	4	US-09-170-996-27	Sequence 27, Appl	
32	48.8	1.4	381	1	US-08-162-081B-38	Sequence 38, Appl	
33	48.8	1.4	381	2	US-08-780-872-38	Sequence 38, Appl	
34	48.8	1.4	381	4	US-09-085-957-38	Sequence 38, Appl	
35	48	1.4	393	1	US-08-162-081B-40	Sequence 40, Appl	
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39	46.8	1.3	3252	4	US-09-677-064-1	Sequence 1, Appl	
40	41.8	1.2	3281	4	US-09-453-702B-85	Sequence 85, Appl	
c	41	38.2	1.1	112132	4	US-09-741-150-3	Sequence 3, Appl
42	36.6	1.0	915	4	US-09-134-001C-1741	Sequence 1741, Appl	
43	36.6	1.0	4211	4	US-09-004-838-106	Sequence 106, Appl	
44	35.2	1.0	731	1	US-08-451-405A-2	Sequence 2, Appl	
45	34.8	1.0	1882	4	US-09-370-253-1	Sequence 1, Appl	

ALIGNMENTS

RESULT 1
US-08-857-076-47
; Sequence 47, Application US/08857076C

; Patent No. 6225120

; GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary

; APPLICANT: Kimura, Koutarou

; APPLICANT: Patterson, Garth

; APPLICANT: Ogy, Scott

; APPLICANT: Paradise, Suzanne

; APPLICANT: Tisenbaum, Heidi

; APPLICANT: Morris, Jason

; APPLICANT: Koweek, Allison

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

; FILE REFERENCE: 00786/351001

; CURRENT APPLICATION NUMBER: US/08/857,076C

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 47

; LENGTH: 3504

; TYPE: DNA

; ORGANISM: Caenorhabditis elegans

US-08-857-076-47

Query Match 100.0%; Score 3504; DB 4; Length 3504;
Best local similarity 100.0%; Pred. No. 0;
Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	CAGATGATGTTAATTTTATCATTCACACACTGCAAGATGCTGAGCAATG	120
DB	61	CAGATGATGTTAATTTTATCATTCACACACTGCAAGATGCTGAGCAATG	120
QY	121	CGAAGAGCCATGCTGAGACCGAGAAATGCGAAGATGCTGCTCGAAATGA	180
DB	121	CGAAGAGCCATGCTGAGACCGAGAAATGCGAAGATGCTGCTCGAAATGA	180
QY	181	GGTGTCCAGATATCATCATATGTCATTCGAGAAATTAAGTAGTATTCGG	240
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QY	241	TGGTTTCTTGAATGTCGCAATCGCTAGAAATCAAGCTATGATTTCAACATCA	300
DB	241	TGGTTTCTTGAATGTCGCAATCGCTAGAAATCAAGCTATGATTTCAACATCA	300

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Db	301	CTTTTCGAATTAATGATTCGTCGCGATGAAGGCGAAACATATTCGCCGTAAGCCACAGATTAT	360
QY	361	GTGTTTCAGACAGAGTTGAATAATTTCCGCGAAATTTGAAGTTATATTTAAAGCATCAACC	420
Db	361	GTGTTTCAGACAGAGTTGAATAATTTCCGCGAAATTTGAAGTTATATTTAAAGCATCAACC	420
QY	421	CTGTGAAATTAAGAGCTCCACGGCACCTTCCCAATGCTTTTCTCTACCAACTGATGGA	480
Db	421	CTGTGAAATTAAGAGCTCCACGGCACCTTCCCAATGCTTTTCTCTACCAACTGATGGA	480
QY	481	ATTAACAGGGATTAAGAAATTAATGATGATTAATGATCAATTCATAGATTAATCACTGAT	540
Db	481	ATTAACAGGGATTAAGAAATTAATGATGATTAATGATCAATTCATAGATTAATCACTGAT	540
QY	541	AAACTGGAAGAGAGCCCTGATGAGGAATCTCGTCAATTCGTGCTTCTCTGAGGCTCGT	600
Db	541	AAACTGGAAGAGAGCCCTGATGAGGAATCTCGTCAATTCGTGCTTCTCTGAGGCTCGT	600
QY	601	ACGAAGAAAACGTGCTTGAACACGTGGAATTAAGGGTACCACTCAACGCGTCCCGAA	660
Db	601	ACGAAGAAAACGTGCTTGAACACGTGGAATTAAGGGTACCACTCAACGCGTCCCGAA	660
QY	661	GACACGTAATCTGTGCTGTGGTGAATTCGTGCCGAAAGTTTGAATCAAAAGTCAAGGCT	720
Db	661	GACACGTAATCTGTGCTGTGGTGAATTCGTGCCGAAAGTTTGAATCAAAAGTCAAGGCT	720
QY	721	GCCAAGCTGAGATTACAGATGTTTGGAGAAAACGTAAAGCGGAAATCAATGAGATTGC	780
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QY	781	GAGAAATATGATGAAGATTCAATTTGAATTCATCCGAACGAACCTCCGAAATCTCTGCTT	840
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QY	1021	GTTGCCCGCAATCTCATGTGCTCTCAAGACATATTTGTCCCGCAAAACCACTTACGAACCA	1080
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Dd	1381	AAATGGATTAAGGAAATGTACACTTTTGAATCTTAATACATGAAGATATGCCACATCTGCA	1440
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Qy	1501	GGTTGGGTAAATATAGTCCCTTAACCGATTTGAGAGATTAACACACAAAGGCAAAATTTT	1560
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Qy	1561	TTCCATCTGTGGGCTCCCTGAACCGACTGCCAATGTGTAGATCGGAGAAAATGAGACA	1620
Dd	1561	TTCCATCTGTGGGCTCCCTGAACCGACTGCCAATGTGTAGATCGGAGAAAATGAGACA	1620
Qy	1621	AGGATAGGCACCAACGACGCGTTACAAATGAAATCTCAAGTTATGTTGAGATTGCA	1680
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Qy	1681	ATGCCGATCAAGACCAATATACATATCTGTCTGACAGCCGAAGTACTTGGACGGAAC	1740
Dd	1681	ATGCCGATCAAGACCAATATACATATCTGTCTGACAGCCGAAGTACTTGGACGGAAC	1740
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Dd	1861	GTCGTGATGTGAGAGATATACATCAAAAGCAGAGCTGATTTGCTCATTTGCTCTCC	1920
Qy	1921	GAACTCGATTTGTGTGACATGATCGTAGAACTTTCCGAGCTCTATGTGATGCTTGA	1980
Dd	1921	GAACTCGATTTGTGTGACATGATCGTAGAACTTTCCGAGCTCTATGTGATGCTTGA	1980
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Qy	2041	CGTGTGATTCGAAAGTTTGACAGTGAGAGTTGATGAGCAGCTGACGCGGTCAATTC	2100
Dd	2041	CGTGTGATTCGAAAGTTTGACAGTGAGAGTTGATGAGCAGCTGACGCGGTCAATTC	2100
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Dd	2401	ATGCCAAAGATGTTGCTACAGATGAACCTGCGTACGAGCTTCGATCGAATTAATCAAA	2460
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Dd	2461	ATGGAATTAATGATTTCTCACTGAGTCTGTGTACAACTGGGTGAATGATATCGAC	2520

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Qy 2701 AACATGATGCTGCTGTTGAACCCGATGAGCTTCTCAATGGGGAATGATGGAAT 2760
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Db 3061 AATCTGATGCTCACTGAAGATGAAGAAATATGCTCAATGATTTGGGTCACATTTGGGA 3120
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Db 3121 CACGGAAGACCAAACTTGGATTCAGGAGATCGTCAACCGTTATTTCTAACCGAACAC 3180
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Db 3361 GATCATTTGAAGAAACCTCTCTTCTGCAATGGAAGAAACCAAGAAAGCGGAAAGTTT 3420
Qy 3421 TTGCTGGAATCTTACGAAGAAAGCTTCTCAATGATGATGATGATGATGATGATGATGAT 3480
Db 3421 TTGCTGGAATCTTACGAAGAAAGCTTCTCAATGATGATGATGATGATGATGATGATGAT 3480
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Db 3481 TTCCACGAGTCAAACTACTGA 3504

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RESULT 2
US-08-162-081B-35

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; Sequence 35, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162, 081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-162-081B-35

Query Match 4.2%; Score 146.4; DB 1; Length 3207;
Best Local Similarity 45.9%; Pred. No. 4.6e-35;
Matches 723; Conservative 0; Mismatches 761; Indels 90; Gaps 3;

Qy 1924 CTCGATTTGTGTGAGTATCGATGAGAACTTTCCGAGCTCTATGATGCTTGAAAA 1983
Db 1708 CTGCTCTGTTAATGAGAACTCTAGAGATGAAATAGTACTGATGCTTGTAAAGAT 1767
Qy 1984 TGAAGCCGCGAGTGTGGACGCGCGCTTGACTTTGCTTGAAACGTTGACGAGATGT 2043
Db 1768 TGGCCTCAATCAAGCTGGAACAGGCTATGAGCTTCTGACGATTAATTAACGATCCT 1827
Qy 2044 GTGATGGAAGTTTGCAGTGTGAGAAAGTGAATGAGACGCTGAGCCGCTGACATTCAT 2103
Db 1828 ATGCTTGAAGTTTGTGCTGCTGCTTGAAGAAATTTTGAACAGATGACAACTTCT 1887
Qy 2104 CTTTTCATATTGCTCTCATACAGGCGTTGAAGTGAAGACCGCGCTCAATCGGAAGTT 2163
Db 1888 CAGTACCTAATTCAGCTAGTACAGTACTAATAATGAAACGATTTTGGATTAACCTGCTT 1947
Qy 2164 GGAATGATGCTCTTGAATGAGCTCTGCGATTAATGAAATGGAATGGAATGGAATGGAAT 2223
Db 1948 GTGAGATTTTATCAAAAAGCGTTAATCAATCAAAAGATCGGCTACTTTTCTTTGG 2007
Qy 2224 CTGCTCCGTGAGAGATTTGCTGCTTGAAGATTTGATCTGAAAGATGAAAGATATCGC 2283
Db 2008 CATTTAAATCTGAGTGAACAAATPAAACAGTATGATGAGATTTGGCTGCTTTGGAG 2067
Qy 2284 CGTATCTACTTGTGATGGAAGTGTACTCTCGTGAATGAAAGACATCAAGATCATC 2343

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Db      3178 CACACATTAAGCA 3191

RESULT 3
US-08-780-872-35
; Sequence 35, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otau, Masayuki; Panayotou, George; Volinia,
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; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
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; COMPUTER READABLE FORM:
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; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780, 872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-35

Query Match 4.2%; Score 146.4; DB 2; Length 3207;
Best Local Similarity 45.9%; Pred. No. 4.6e-35;
Matches 723; Conservative 0; Mismatches 761; Indels 90; Gaps 3;

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 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-162-081B-34

Query Match 3.7%; Score 130; DB 1; Length 3240;
 Best Local Similarity 45.7%; Pred. No. 6,2e-30;
 Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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 1984 TGGAAACCGCGAGTGTGCGACCGCGTTGACTTTGCTTGAATAAGTTGACGATCGT 2043
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 1888 CAGTATTTAATCTACCTAGTACAGGCTCTAAATATGAAATATTTGATTAATCTTCTT 1947
 2164 GGAATGATGCTCTTACTAGAGCTCTCTGCGATTAATGAAATGAGCAATGACTTTCTG 2223
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 2641 CTCAAAAGCAAGAAACAAAGAGAAATATATGATGAGCCATTGACCTGTTTACAGTTCA 2700
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 3424 GCTGAAATCTAGAGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 3483
 3118 ATGAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3177
 3484 CACGAGTCAACA 3497
 3178 CACACATTAACA 3191

RESULT 6

US-08-780-872-34

Sequence 34, Application US/08780872

Patent No. 5846824

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu

APPLICANT: Hales, Waterfield, Michael Derek; Parker, Peter

APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,

APPLICANT: Stefano, Gout, Ivan Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESS: Felife & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/780,872
 FILING DATE: 09-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/162,081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-780-872-34

Query Match 3.7%; Score 130; DB 2; Length 3240;
 Best Local Similarity 45.7%; Pred. No. 6.2e-30;
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QY 1924 CTCGCATTGTGTGAGCATGATCGTGAAGAACTTTCCGACCTCATGTGATGCTTGAAGAAA 1983
 DB 1708 CTGTCTGTTAAATGGAATCTAGAGATGAAGTAGCCAGATGATTCGTGTAAGAAAGAT 1767
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 DB 3118 ATGAACAATAATGAATGATGACATCATGTGTGCTGAACAAATAATGATTTGATCTTC 3177
 QY 3484 CACGAGTCAACA 3497
 DB 3178 CACACATTAACA 3191

RESULT 7
 US-09-085-957-34

Sequence 34, Application US/09085957
Patent No. 6274327
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Oden, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
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TITLE OF INVENTION: THEIR PREPARATION AND USE
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STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
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REFERENCE/DOCKET NUMBER: LUD 5256
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INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-34

Query Match 3.7%; Score 130; DB 4; Length 3240;
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QY 1984 TGGAAACCGCGAGTGTGCGACGCGCTTGAAGCTTGTGGAAGAACTTGAACGATGCT 2043
DB 1768 TGGCTCTCAATCAACCTGAACAGGCTTATGAACTTGTGACTGTAATTAACCAATCT 1827
QY 2044 GTGATTGCAAGATTGCAAGTGAAGATGATGAGCAGTGAAGCCGCTCATTTCCAT 2103
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DB 1888 CAGATTATTAATTCAGCTAGTGAAGTCTTAAATATGAACAATATTTGATTAATCTTCT 1947
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DB 1948 GTGAGATTTTATCTGAAGAAAGCATGACTATTAAGAAAGATGGGCACTTTTCTTTGG 2007
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 ; Sequence 32, Application US/08162081B
 ; Patent No. 5824492
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu
 ; APPLICANT: Bala, Waterfield, Michael Derek, Parker, Peter
 ; APPLICANT: Joseph, Otsu, Masayuki, Panayotou, George, Volinia,
 ; APPLICANT: Stefan, Gout, Ivan Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/162,081B
 ; FILING DATE: February 7, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/00761
 ; FILING DATE: 13 April 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pasqualini, Patricia A.
 ; REGISTRATION NUMBER: 34,894
 ; REFERENCE/DOCKET NUMBER: LUD 5256
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3412 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single or double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3204
 ; OTHER INFORMATION: /standard_name="CDS"
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 Best Local Similarity 45.7%; Pred. No. 6.4e-30;
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RESULT 9 US-08-780-872-32

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; Sequence 32, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Discrete, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 32:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name="CDS"
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Query Match      3.7%; Score 130; DB 2; Length 3412;
Best Local Similarity 45.7%; Pred. No. 6.4e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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; Sequence 32, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek, Parker, Peter
; APPLICANT: Joseph, Oseu, Masayuki, Panayotou, George, Volinia,
; APPLICANT: Stefano, Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2

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OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"
US-09-085-957-32

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Query Match 3.7%; Score 130; DB 4; Length 3412;
Best Local Similarity 45.7%; Pred. No. 6.4e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;
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Db      2881 TTAATATGATTAAGAAAGAGCCCAAGATGACAAAGAGAAATTTGAGAGTTT 2940
Qy      3244 AAAAGCTATGCTGAGAGCTTCAAGATGATGATGATGATGATGATGATGATGATGAT 3303
Db      2941 CAGGAGATGTGTTAAGAGCTTATCTAGCTATTCACAGCATGCCAATCTTTCATTAAT 3000
Qy      3304 TTGTTACCTTGATGCTGGAATGAGATGCTGAGCTGTGAGCAAGAGCGGATTTGAT 3363
Db      3001 CTTTTCATATATGCTTGTGCTGATGATGCAAGATCAATCTTTGATGATGATGATGAT 3060
Qy      3364 CATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAG 3423
Db      3061 TACATTCAGAAAGCCCTAGCCTTAGTA---AACTGAGCAAGAGGCTTTGAGATTTT 3117
Qy      3424 GCTGATATCTAGAGAGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGAT 3483
Db      3118 ATGAACCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3177
Qy      3484 CACGAGTCAACA 3497
Db      3178 CACACATTAACA 3191

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RESULT 11

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US-09-357-070-1
; Sequence 1, Application us/09357070
; Patent No. 6046049
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 DELTA EXPRESSION
; FILE REFERENCE: RTS-0076
; CURRENT APPLICATION NUMBER: US/09/357,070
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(3331)
US-09-357-070-1

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Query Match      3.0%; Score 103.6; DB 3; Length 3868;
Best Local Similarity 53.7%; Pred. No. 1.2e-21;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

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Qy      3000 CTCGTGTTGATTAATTCAGTTGCCAGTACATTAATGGAATTCAGATTCGACAGTGA 3059
Db      2827 CTCCTGTGCTGCTATTTGTGTGCGCACATATGTGCTGGCATTTGGCGATCGGACAGCA 2886
Qy      3060 TAATGTATGCTCACTGAAGATGAGAAATATGTCATATGATTTGCTGATATTTGGG 3119
Db      2887 CAACATCATATGATCCAGAGAGAGTGGGACGTGTCACATTTGATTTTGGCATTTCTGGG 2946
Qy      3120 ACAGGAAAGCAAACTTGGATTCAGAGATGATGATGATGATGATGATGATGATGATGAT 3179
Db      2947 GAATTTCAAGCCAAAGTTGAAATCAACCGGAGGTGTCCATTCATCTTCACTACGA 3006
Qy      3180 CTTTATGACAGTATTCATCGAGGTAATCTGTGATGAAATTCGATGAGCTCAAAA 3239
Db      3007 CTTTGTCCATGATGATTCAGCAGGGAA-----GACTAATATATGATGAAATTTGAAAG 3060
Qy      3240 ATTCAAAAGTTATGCTGCAAGGCTTACAGAAATATGTAATTAATGAGATTTTGTGT 3299
Db      3061 GTTCCGGGGCTATCTGTGAAGAGGCGCTTACACCATCTGCGGGCGCCAGGCTTCTTCT 3120
Qy      3300 TTCTTGTTCACCTTGAATGCTGGAATGATGATGATGATGATGATGATGATGATGAT 3359
Db      3121 CCACCTCTTGTCCCTGATGCGGGCGGAGGCTGTGATGCTCAGCTCTCCAAAGCAT 3180
Qy      3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAGAGAGAGAG 3419
Db      3181 CCAATATCTCAAGAGCTCC---TGGCACTGGGAAACAGAGAGAGAGAGAGAGAGAG 3237
Qy      3420 TTTGCTGGAATCTACAGAGAGAGCTTCAATGATGATGATGATGATGATGATGATGATGAT 3479
Db      3238 CTTCCGAGTGAAGTTAAGAGAGAGCTCCGTAAGAGCTGGAAGAGAGAGAGAGAGAGAG 3297
Qy      3480 CTTCCAGCAGT 3491
Db      3298 GGGCCCAACAAGT 3309

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RESULT 12
US-08-777-405A-1
; Sequence 1, Application us/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chanley, David
; APPLICANT: Hoekeira, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

```

STREET: 6300 Sears Tower/233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/777,405A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 585873and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/33441
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5220 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 196..3327
 US-08-777-405A-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;
 Best Local Similarity 53.7%; Pred. No. 1.5e-21;
 Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

3000 CTCGCTGTGATGATTCAGTGGCCGATACATATGGAATTCAGAGATCGTCACAGTGA 3059
 2826 CTCCTGTGCTGATGATGATGCGCCATATGCTGGCGATTGGCGATGGCAGCGCA 2885
 3060 TAATCGATGCTCAGTGAAGTGAATAATGTCACATTGATTTGGTCACTTTGGG 3119
 2886 CAACATCATGATCCGAGAGAGTGGGAGAGCTGTTCCATTGATTTGGCATTCTGGG 2945
 3120 ACACGGAAGACCAAACTTGGGATCCAGGAGATGCTCAACCGTTTATTTAAACGACA 3179
 2946 GAATTTCAAGACCAAGTTTGAATCAACCGGAGCTGTCCCTCATCTCATCTATGA 3005
 3180 CTTTATGACAGTATTCGATCGGCTAACTGTGATGGAATTCGATGAGTACAAAA 3239
 3006 CTTTGTCCATGATTCACAGGGGAA-----GACTAATTAATGAGAAATTTGAACG 3059
 3240 ATTCAAAAGTTATGCGTGAAGCTTACGAAAGTATGTAATTCAGATTTGTTGCT 3299
 3060 GTTCCGGGGCTACTGTGAAGAGGCTTACACATCTCTCGCGCCAGCGCTTCTTCTCT 3119
 3300 TTCCTGTTCACCTGATGCTGGAAATGAGATTGCTGAGCTGTGACGAAAGCGGATTT 3359
 3120 CCACCTCTTTCCTGATGCGGGGCGGAGCGCTGCTGAGCTGCTCCAAAGACAT 3179
 3360 GGAATCATTTGAAGAAACCTCTTTCGCAATGGAAGCAAGAAAGAGCGGAAGTT 3419
 3180 CCGATATCTCAAGACTCC--TGGCATGGGGAAGAGAGAGAGCACTGAAGA 3236
 3420 TTTCCGTGAATTCAGAAAGAGCTTCAATGATGATGCTTACCAAAAGCAATTTGGCT 3479
 3237 CTTCCGAGTGAATTTAAGCAAGCCTCCTGTGAGACTGGAAGAACCAAGTGAATGCGCT 3296
 3480 CTTCAAGCAGT 3491
 3297 GGCCCAACAAGT 3308

RESULT 13
 US-08-977-871A-1
 Sequence 1, Application US/08977871A
 Patent No. 5882910
 GENERAL INFORMATION:

APPLICANT: Chantry, David
 APPLICANT: Hoekstra, Merl F.
 APPLICANT: Holtzman, Douglas A.
 TITLE OF INVENTION: No. 5882910el lipid Kinase
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
 STREET: 6300 Sears Tower/233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,871A
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/777,405
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5882910and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/33441
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5220 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 196..3327
 US-08-977-871A-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;
 Best Local Similarity 53.7%; Pred. No. 1.5e-21;
 Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

3000 CTCGCTGTGATGATTCAGTGGCCGATACATATGGAATTCAGAGATCGTCACAGTGA 3059
 2826 CTCCTGTGCTGATGATGATGCGCCATATGCTGGCGATTGGCGATGGCAGCGCA 2885
 3060 TAATCGATGCTCAGTGAAGTGAATAATGTCACATTGATTTGGTCACTTTGGG 3119
 2886 CAACATCATGATCCGAGAGAGTGGGAGAGCTGTTCCATTGATTTGGCATTCTGGG 2945
 3120 ACACGGAAGACCAAACTTGGGATCCAGGAGATGCTCAACCGTTTATTTAAACGACA 3179
 2946 GAATTTCAAGACCAAGTTTGAATCAACCGGAGGTTCCATTTCATCTCATCTATGA 3005
 3180 CTTTATGACAGTATTCGATCGGCTAACTGTGATGGAATTCGATGAGTACAAAA 3239
 3060 GTTCCGGGGCTACTGTGAAGAGGCTTACACATCTCTCGCGCCAGCGCTTCTTCTCT 3119
 3300 TTCCTGTTCACCTGATGCTGGAAATGAGATTGCTGAGCTGTGACGAAAGCGGATTT 3359
 3120 CCACCTCTTTCCTGATGCGGGGCGGAGCGCTGCTGAGCTGCTCCAAAGACAT 3179
 3360 GGAATCATTTGAAGAAACCTCTTTCGCAATGGAAGCAAGAAAGAGCGGAAGTT 3419
 3180 CCGATATCTCAAGACTCC--TGGCATGGGGAAGAGAGAGAGCACTGAAGA 3236
 3420 TTTCCGTGAATTCAGAAAGAGCTTCAATGATGATGCTTACCAAAAGCAATTTGGCT 3479
 3237 CTTCCGAGTGAATTTAAGCAAGCCTCCTGTGAGACTGGAAGAACCAAGTGAATGCGCT 3296
 3480 CTTCAAGCAGT 3491
 3297 GGCCCAACAAGT 3308

Db 3060 GTTCGGGGCTACTGTGAAGGGCCTACACCATCTCGCGCGCCACGCGCTTCTCTTCT 3119
Qy 3300 TTCTTGTTACCTTGATGCTGGAATGGAATTGCTGAGCTGTGAGAGAAAGCGATT 3359
Db 3120 CCACCTCTTTCCTGATGCTGGCGGCGGACGCTGCTGAGCTGTGCTCCAAAGACAT 3179
Qy 3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAAAGTT 3419
Db 3180 CCAGTATCTCAAGAGCTCCC--TGGCACTGGGGAAGAAAGAGAGAGAGCACTGAAGA 3236
Qy 3420 TTTCCTGGAATCTCAAGAGAGCTTCAATGATCATGCTTACCAAAAGCAATTGGCT 3479
Db 3237 CTTCGAGTGAAGTTTAAGAGAGCCCTCGTGAAGCTGGAAGAAACCAAGTGAAGTGGCT 3296
Qy 3480 CTTCACGCACT 3491
Db 3297 GGCCCAACAGT 3308

RESULT 14

US-09-225-951-1
; Sequence 1, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoeckstra, Merl F.
; APPLICANT: Holzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5220 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..3327
; US-09-225-951-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;
Best Local Similarity 53.7%; Pred.No. 1.5e-21;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;
Qy 3000 CTCGCTGTGGATTTTCACTTCCACGACATATGGAATCAAGAGATGTCACAGTGA 3059
Db 2826 CTCCTGTCTGGCTATGTGTGGCCACATATGTCTGGGCAATTGGCGATCGCACAGCGA 2885

Qy 3060 TAATCTAGTCTCACTGAAGATGGAATAATGTCCATATTGATTTTCGTACATTTTGGG 3119
Db 2886 CAACATCATGATCCGAGAGAGTGGCAGCTGTTCACATTTGATTTTGGCACTTTCTGGG 2945
Qy 3120 ACACGAAAGACCAACTTTGGGATCCAGCGAGATGTCAACCGTTTATTCTAACGACA 3179
Db 2946 GAATTTCAAGACCAAGTTTGAATCAACCGGAGCGTGTCCATTCATCTCACCTATGA 3005
Qy 3180 CTTTATGACAGATGATGATGGGTAATCTGTGATGGAATAATTCGATGAGCTACAAA 3239
Db 3006 CTTTGTTCATGATGATTCAGCAGGGGAA-----GACTAATTAATGATGAATTTGAACG 3059
Qy 3240 ATTCAAAAGTATGCTGCAAGCCTTCAAGATGATGATGATTAATTCAGATTTTTCGT 3299
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Db 3120 CCACCTCTTTCCTGATGCTGGCGGCGGACGCGCTGCTGAGCTCAAGCTCCAAAGACAT 3179
Qy 3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAAAGTT 3419
Db 3180 CCAGTATCTCAAGAGCTCCC--TGGCACTGGGGAAGAAAGAGAGAGAGCACTGAAGA 3236
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Db 3237 CTTCGAGTGAAGTTTAAGAGAGCCCTCGTGAAGCTGGAAGAAACCAAGTGAAGTGGCT 3296
Qy 3480 CTTCACGCACT 3491
Db 3297 GGCCCAACAGT 3308

RESULT 15

US-08-916-917-3
; Sequence 3, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Brabelmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

LENGTH: 3808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-917-3

Query Match 2.8%; Score 96.4; DB 2; Length 3808;
Best Local Similarity 51.9%; Pred. No. 2.1e-19;
Matches 270; Conservative 0; Mismatches 241; Indels 9; Gaps 2;

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DB 2844 AAAAGTTTCAGGACGCTGGAGAGATTTGTTATTCCTGTGCGGCTACTGTGTGCAA 2903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3026 CGTACATATGGGATCAAGATCGTCAAGATGATATCTGATGCTCACTGAAGATGGA 3085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2904 CTTTGTCTCGAATAGGCGACAGACAAATGACAAATATTAATGATCTCAGAAACAGAA 2963
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3086 AATATGTCACATTTGATTTGGTCACTTTGGGACACGGAAGAACCAACTTGGGATCC 3145
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DB 2964 ATCTATTTCAATTTGATTTGGACACATTTCTGGAAATTAACAAGTTTCTGGGCATTA 3023
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3146 AGCGAGATCGTCAACCGTTTATTTCTAACGGAACCTTTATGACAGTATTCGATCGGTA 3205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3024 ATAAAGAGAGGGTGCATTTGTGCTAACCCAGACTTCTGTGTGTGAT-----GGGA 3077
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QY 3206 AATCTGTGATGGAATTCGCATGAGCTACAAAATTCAAAAGTTATGCTGGAAGCT 3265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3078 CTTCTGGAAGAAGACAGAGCTACACTTCAGAAATTTCAAGATGTGCGTCAAGGCTT 3137
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QY 3266 AGGAAGTAAATGGAATTAATCGAGATTTGTCGTTTCTTGTTCACCTTGATGCTGGAA 3325
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DB 3138 ACTTACCCCTTGTCTATCAACAACCTTACTGATCCTCTTCTTCATGATGCTGATGA 3197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3326 TGGAGTTGCTGAGCTGCGAGAAAGCGAATTTGATCATTTGAAGAAACCTCTTCT 3385
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DB 3198 CAGGAATGCCCCAGTTAACGCAAGAGAATGATTAAGATATTTCTGATTCAGATTGA 3254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3386 GCAATGGAAGAAAGCAAGAAAGAGCAAGAAAGTTTTCGCTGAATCTACGAAGAGCT 3445
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DB 3255 CAGTGGGCAAAAGTGAGAGAGTGTAAAGATATTTCTGATTCAGATTGAAGTTTGA 3314
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QY 3446 TCAATGATCATGCTTACCAAAACGAATTTGGCTTTCCA 3485
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DB 3315 GAGACAAAGATGACCGTGCAGTTTAACTGTTCTTACA 3354
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Job time : 256 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: June 6, 2003, 02:28:44 ; Search time 453 Seconds
(without alignments)
10825.561 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504
Sequence: 1 CGGAAGCCATGAGCTCGAG.....ACGAGTCACACTACTGTA 3504

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	103.6	3.0	3387	9	US-10-162-160-2
4	103.6	3.0	5220	9	US-10-027-591-1
5	77	2.2	5990	10	US-09-917-800A-477
6	68.6	2.0	5061	12	US-10-092-219-1
7	64	1.8	339	9	US-09-796-692-7359
8	64	1.8	339	9	US-10-040-862-7359
9	59	1.7	326	9	US-09-796-692-7451
10	59	1.7	326	9	US-10-040-862-7451
11	46.8	1.3	3252	10	US-09-921-232-1
12	46.8	1.3	3252	10	US-09-921-330-1
13	46.8	1.3	3252	10	US-09-921-329-1
14	42.8	1.2	2418	10	US-09-771-161A-10
15	42.2	1.2	5703	10	US-09-801-368-389
16	41.8	1.2	3281	9	US-10-114-170-85
17	41.2	1.2	4074	10	US-09-764-877-3796
18	41	1.2	302	9	US-09-925-299-710
19	41	1.2	302	10	US-09-925-299-710

20	41	1.2	2620	10	US-09-925-302-205	Sequence 205, App
21	41	1.2	11812	9	US-10-239-676-210	Sequence 210, App
22	40	1.1	464	9	US-09-918-995-32689	Sequence 32689, A
23	39.4	1.1	466	9	US-09-918-995-35578	Sequence 35578, A
24	38.6	1.1	2000	9	US-09-938-842A-5006	Sequence 5006, App
25	38.6	1.1	2002	10	US-09-887-576-4	Sequence 4, Appl1
26	38.6	1.1	640681	10	US-09-790-988-1	Sequence 264, App
27	38	1.1	532	9	US-10-184-644-264	Sequence 264, App
28	38	1.1	532	9	US-10-184-634-264	Sequence 264, App
29	37.8	1.1	436	9	US-09-918-995-857	Sequence 857, App
30	37.8	1.1	7864	10	US-09-834-575-805	Sequence 805, App
31	37	1.1	6071	9	US-10-233-676-78	Sequence 78, Appl1
32	36.4	1.0	867	9	US-10-123-155-20	Sequence 20, Appl1
33	36.2	1.0	364	10	US-09-960-352-10067	Sequence 10067, A
34	36	1.0	2432	9	US-10-198-846-12893	Sequence 12893, A
35	36	1.0	4000	9	US-09-981-353-8	Sequence 8, Appl1
36	35.8	1.0	408	10	US-09-960-352-1221	Sequence 1221, App
37	35.8	1.0	494	9	US-09-918-995-19234	Sequence 19234, A
38	35.6	1.0	446	9	US-09-918-995-24787	Sequence 24787, A
39	35.6	1.0	515	9	US-10-066-543-1214	Sequence 1214, App
40	35.6	1.0	1955	9	US-09-984-271-98	Sequence 98, Appl1
41	35.6	1.0	1955	9	US-09-813-153-80	Sequence 80, Appl1
42	35.6	1.0	2550	9	US-09-813-153-65	Sequence 65, Appl1
43	35.6	1.0	2971	9	US-09-984-271-37	Sequence 37, Appl1
44	35.6	1.0	13606	9	US-10-239-676-165	Sequence 165, App
45	35.4	1.0	419	10	US-09-960-352-11234	Sequence 11234, A

ALIGNMENTS

RESULT 1

US-09-205-658-47
Sequence 47, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICATOR: Osg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: US/09/205, 658
EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888, 534
EARLIER FILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US98/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 3504
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-09-205-658-47

Query Match 100.0%; Score 3504; DB 10; Length 3504;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 US-09-844-353A-47
 ; Sequence 47, Application US/09844353A
 ; Patent No. US20020037585A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruvkun, Gary
 ; APPLICANT: Kimura, Koutarou
 ; APPLICANT: Patterson, Garth
 ; APPLICANT: Ogg, Scott
 ; APPLICANT: Paradise, Suzanne
 ; APPLICANT: Morris, Jason
 ; APPLICANT: Kowsek, Allison
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
 ; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 ; FILE REFERENCE: 00786/351005
 ; CURRENT FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 08/857,076
 ; PRIOR FILING DATE: 1997-05-15
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 3504
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 US-09-844-353A-47
 Query Match 100.0%; Score 3504; DB 10; Length 3504;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3301 TCCCTGTTCACTTATGCTCGGAATGAGATGCTGAGCTGTGACGAAACGGAATTTG 3360
Qy 3361 GATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAACGGAAGTTT 3420
Db 3361 GATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAACGGAAGTTT 3420
Qy 3421 TTCGCTGAATCTACGAAGAGCCTTCAATGATCATGCTTACCAAAACGAATTTGCTC 3480
Db 3421 TTCGCTGAATCTACGAAGAGCCTTCAATGATCATGCTTACCAAAACGAATTTGCTC 3480
Qy 3481 TTCCACGAGTCACAACTACTACGA 3504
Db 3481 TTCCACGAGTCACAACTACTACGA 3504

```

```

RESULT 3
US-10-162-160-2
; Sequence 2, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
; APPLICANT: Van Hasebroeck, Bart
; APPLICANT: Macerfeld, Michael D.
; TITLE OF INVENTION: No. US20030099627A1el Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 2
; LENGTH: 3387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-160-2

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Query Match 3.0%; Score 103.6; DB 9; Length 3387;
Best Local Similarity 53.7%; Pred. No. 1,1e-18;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

```

```

Qy 3000 CTCGTGTGTAATTCAGTTGCCACGATCATATGGAATCAAGATCGTCAAGTGA 3059
Db 2631 CTCCTGTGCTGCTATGTTGTGCGCACATATGTGCTGGCATTTGGCCATCGACGA 2690
Qy 3060 TAATCTGATGCTCACTGAAGATGAAATATGTTCCATTTGATTTGCGTCAATTTGGG 3119
Db 2631 CAACATCATGATCCAGAGAGTGGGACACTGTCCACATGATATTTTGGCCATTTCTGGG 2750
Qy 3120 AACGGAAGAACCAACTTGGGATCCAGGAGATTCGTCAACCGTTATTTTACCGAACAC 3179
Db 2751 GAATTTCAAGACCAAGTTGGAATCAACCGGAGGCTGTCCATTCATCTCCTACGA 2810
Qy 3180 CTTATGACAGTATTCGATCGGGTAATCTGTGATGGAATTTGCGATGAGTCAACAAA 3239
Db 2811 CTTTGTCCATGATGATTCAGCAGGGGAA-----GACTATATATGTAAGAAATTTGAAAG 2864
Qy 3240 AATCAAAACGTTATGCGTGAAGCCTTACGAGATATGATGATTTGCTTGTCT 3299
Db 2865 GTTCGGGGCTATCTGTGAAGAGGCTTACCAATCTGTGGGGCCACGCGGCTTCTTCTCT 2924
Qy 3300 TTCTTGTTCACCTTATGCTCGGAATGAGATGCTGAGCTGTGACGAAAGCGGATTT 3359
Db 2925 CCACCTCTTGTGCTGATGCGGGGCGGACGCGCTGTCTAGCTCAGCTCTCCAAAGACAT 2984
Qy 3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAACGGAAGTTT 3419
Db 2985 CCAGATATCTCAAGGACTCCC---TGGCACTGGGGGAAACAGAGGAGGACTGAACCA 3041
Qy 3420 TTTGCTGGAATCTACGAAGAGCCTTCAATGATCATGCTTACCAAAACGAATTTGCT 3479
Db 3042 CTTCCGATGTAAGTTTAAAGAACCCCTCTCGTAGAGCTGGAACCAAGTGAATGCTGCT 3101
Qy 3480 CTTCCAGCAGCT 3491
Db 3102 GACCCACAAAGCT 3113

```

```

RESULT 4
US-10-027-591-1
; Sequence 1, Application US/10027591
; Patent No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
US-10-027-591-1

```

Query Match 3.0%; Score 103.6; DB 9; Length 5220;
Best Local Similarity 53.7%; Pred. No. 1.5e-18;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

3000 CTCGATGTTGATATTCAGTTCACCGACGACATTAATGGGATCAAGGATGTCACAGTGA 3059
2826 CTCCTGCTGCTGCTATTTGTCGACATATGCTGCGCATTTGGCGATGGCAGACGCA 2885
3060 TAATCTGATGCTCAGTGAAGATGAAATATGTCCACATTTGCGTACATTTTGGG 3119
2886 CAACATCATGATCCGAGAGAGTGGGAGCTGTTCCACATTTGATTTGGCATTCTCTGG 2945
3120 AACGAGAAAGACCAAACTGGGATCCAGGAGATGTCAACGTTTATTTCAACGAGACA 3179
2946 GAATTTCAAGCCAAAGTTTGAATCAACCGGAGCGGTGTCATTCATCTCACCTATGA 3005
3180 CTTTATGACGATGATTCGATCGGATTAATCTGTGATGGAATTCGATGAGCTACAAA 3239
3006 CTTTGTCTGATGATTCAGACAGGGGAA-----GACTAATTAATGAGAAATTTGACG 3059
3240 ATTCAAAAGCTTATGCGTGAAGCCCTACGAGTAAATGGAATTCAGATTTGCTGT 3299
3060 GTTCCGGGCTACTGTGAAGGAGCCCTACACATCTCGCGGCGCAGCGGCTCTCTCT 3119
3300 TTCTTTGCTACCTTGATGCTGGGAATGAGATTCCTGCTGTGACGAGAAAGCGATTT 3359
3120 CCACCTCTTTCCTGATGAGGCGGCGGAGGCTGCTGAGCTGAGCTGCTCAAAAGACAT 3179
3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAGAAACAAAGAGAGAGAAAGTT 3419
3180 CAGATCTCAAGGAGCTCC---TGGCATCTGGGAGAAACAGAGAGAGAGACTGAAGA 3236
3420 TTTCGCTGAATCTACAGAAAGCTTCAATGATGATGCTCTACCAAAAGCAATTTGCT 3479
3237 CTTCGAGTGAAGTTTAAAGAGCCCTCGTGAAGCTGAGAAACCAAGTAAAGTGGCT 3296
3480 CTTTCAAGGAGT 3491
3297 GGCCCAACAAGT 3308

RESULT 5

US-09-917-800A-477
Sequence 477, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castile, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 477

LENGTH: 5990
TYPE: DNA

ORGANISM: Rattus norvegicus

OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477

Query Match 2.2%; Score 77; DB 10; Length 5990;
Best Local Similarity 50.1%; Pred. No. 7.8e-11;
Matches 253; Conservative 0; Mismatches 240; Indels 12; Gaps 2;

2924 AAATCCCATCGAAGAAAGATGTAATTAATCAAGCCATGAAGAAATATTTGAAAGTG 2983
3262 AAACACCATCAAGAAAGTTCAGTCAAGCAACACTTAAGAAAGATTAATGAAAGG 3321
2984 TCGATCG--ATTCTATATCTGCTGTGTTGGATATTCAGTTCCACGACATTAATGGAA 3040
3322 CTTTGAAGAACTTTTATCTTGTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3381
3041 TCAAGATGTCACAGTATATCTGATGCTCACTGAAGATGAAATATATGTCCACATTTG 3100
3382 TCTGTACCGACATATATACATATATCTGACAAAGTCAAGCCACATGTTTCAATTTG 3441
3101 ATTTCGTCACATTTTGGGACACGGAAGACCAAACTTGGATCCAGGAGATGCTAAC 3160
3442 ACTTTGAAAAATCTTGGGTACGCAACAAATTTGGCGGTATTAAGAGGAGCGAGCGC 3501
3161 CTTTATTTCTAACGACACATTTATGACAGATTCGATTCGGGTAAATCTGTGATGGA 3220
3502 CTTTATTTTAACTTCAAGATGAGATCTTATTTTACGAGAGGT-----GGGAAAA 3552
3221 ATTGCATGAGCTACAAATTTCAAAACGTTATGCGTGAAGCTTACGAGATTAATGTGA 3280
3553 ACACACAGATTTTAAAGCTTTCGGAACCTGTGTGAAGGCTTCAACATTTGTGAGGA 3612
3281 ATTAATGAGATTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3340
3613 AGCAGAGCACTGCTCTGAGCCTTCTGAGAAATGATCTGATCCCGGCTCTCTGAGC 3672
3341 TGTCAAGCAAGCGATTTGATCATTTGAAGAAACCTCTTCTGCAATGAGAGAAACA 3400
3673 TGAGGGGATTTGAAGACCTGAAATTCGTACAGCAATCTCGGCCACAGACAGACC 3732
3401 AAGAGAGCGAGAAAGTTTTCGC 3425
3733 TGAGAGCCACAAGTCAATTTTACAC 3757

RESULT 6

US-10-092-219-1
Sequence 1, Application US/10092219
Patent No. US20020115114A1
GENERAL INFORMATION:
APPLICANT: Damin, Jan
TITLE OF INVENTION: No. US20020115114A1 Lipid kinase
FILE REFERENCE: 1064HG/50947
CURRENT APPLICATION NUMBER: US/10/092,219
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: PCT/GB98/00244
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/355,160
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 9701652.1
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent In version 3.1
SEQ ID NO 1
LENGTH: 5061

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1
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Query Match      2.0%; Score 68.6; DB 12; Length 5061;
Best Local Similarity 51.9%; Pred. No. 1.9e-08;
Matches 179; Conservative 0; Mismatches 164; Indels 2; Gaps 1;
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QY 2865 GATTCGGAACATCGGAATGAGATGAGAAAGAAAGCAAAAGSACTACCAA 2924
DB 3565 GCTTCGATACCCCTCAGGAAATCCAGTGAATGTGTGACAGATCCTTTAAAGT 3624
QY 2925 AATTCATCGAAAAGAAATGATTAATCTCAAGCCATGAAAGAAATTTGAAAGTGT 2984
DB 3625 AAACCACTGCAAGATGCTAAAGAAATCAATCCCTCGAAGAAATATGAAAGGCT 3684
QY 2985 CGATCGA--TTCCATACCTCGGTGGTGGATTAATGATTCAGTTGCCAGTACATATGGGAATC 3042
DB 3685 TCAGGAACCTTAATTAATTCCTGCTGAGTGTGTAGCCACTATGTTTAAAGCATC 3744
QY 3043 AAGGATCGTCAAGATTAATCTGATGCTCACTGAAGATGAAATATATGTCACATTTGAT 3102
DB 3745 TGTATGACACAAATGACATTAATGCTTGAACACAGGAGACATGTTTCAATTTAC 3804
QY 3103 TTCGTCACATTTTGGGACACGAAACCAAACTTGGATCCAGCGAGATGTCACCG 3162
DB 3805 TTTGGAAGTTTGGGACATGACAGATGTTTGGCAGCTTCAAAAGGATGGGCTCCT 3864
QY 3163 TTTATCTAACGGAACACTTATGACAGTATGATTCATGGGATAA 3207
DB 3865 TTGTGCTGACCTCTGATATGGCATATATGTCATTAATGGGGTGAA 3309
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RESULT 7

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US-09-796-692-7359/C
; Sequence 7359, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
```

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; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7359
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-7359
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Query Match      1.8%; Score 64; DB 9; Length 339;
Best Local Similarity 58.3%; Pred. No. 6.6e-08;
Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
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QY 2610 TGCATGATCTTCAAGATGAGACGATCTGCGCAGACATGCTTGTCTCAAGTCT 2669
DB 193 TGAGTGTATTTTAAATATGATGATTTACGACAGATATGTTGACATCCCAATGTT 134
QY 2670 CGAAGTTATGATTAATCTGGAAGGCTGCAAACTGATGCTGTTGAAACCCGTACGC 2729
DB 133 GCGCTTATGATTTACTCTGAAAGAGCTGTTGATCTTGGAGATGTTGCCCTATGG 74
QY 2730 AGTTCTTCATGAGGAGAAATGATTTGAATTTGAAGTTGCTTAATGTAACCAAT 2789
DB 73 CTGTTAGCAACAGAGATCGCTCTGCGCTCATTTGAAGTTGAGCACCTTGAAACAAT 14
QY 2790 AATCGAGATCA 2801
DB 13 TGCTGACATTTCA 2
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RESULT 8

```
US-10-040-862-7359/C
; Sequence 7359, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 7359
LENGTH: 339
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-862-7359

Query Match 1.8%; Score 64; DB 9; Length 339;

Best Local Similarity 58.3%; Pred. No. 6,6e-08; Mismatches 80; Indels 0; Gaps 0;

Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGACGATCTTCCGAGACGCTGTTCTTCAAGTTCT 2669
DB 133 TGGAGTGAATTTTAAAAATGGATGATTTACGACAGATATGTTGACACTCAATGTT 134
QY 2670 CGAAGTTATGATTAACATCTGGAAGGCTGCAACATTTGCTGTTTGAACCCGTACGC 2729
DB 133 GCGCTTGAATGATTTACTCTGGAAGAACGCTTGTGATCTTCGATGCTCTTATG 74
QY 2730 AGTTCTCCATGGAGAAATGATTTGATTTAGTTGCTTAATTTAAACAT 2789
DB 73 CTGTTTACACAGAGATGCTGCTGCTCATTTGAAGTTGAGCACTCTGAACAT 14
QY 2790 ATTCGATGATCA 2801
DB 13 TCGTGACATTC 2

RESULT 9

US-09-796-692-7451/c

Sequence 7451, Application US/09796692

Publication No. US20020198362A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

PRIOR FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7451

LENGTH: 326

TYPE: DNA

ORGANISM: Homo sapiens

US-09-796-692-7451

Query Match 1.7%; Score 59; DB 9; Length 326;

Best Local Similarity 58.1%; Pred. No. 1.8e-06; Mismatches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGACGATCTTCCGAGACGCTGTTCTTCAAGTTCT 2669
DB 180 TGGAGTGAATTTTAAAAATGGATGATTTACGACAGATATGTTGACACTCAATGTT 121
QY 2670 CGAAGTTATGATTAACATCTGGAAGGCTGCAACATTTGCTGTTTGAACCCGTACGC 2729
DB 120 GCGCTTGAATGATTTACTCTGGAAGAACGCTTGTGATCTTCGATGCTCTTATG 61
QY 2730 AGTTCTCCATGGAGAAATGATTTGATTTAGTTGCTTAATTTAAACAT 2789
DB 60 CTGTTTACACAGAGATGCTGCTGCTCATTTGAAGTTGAGCACTCTGAACAT 2

RESULT 10

US-10-040-862-7451/c

Sequence 7451, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/040,862

PRIOR FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10467

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7451

LENGTH: 326

TYPE: DNA

ORGANISM: Homo sapiens

US-10-040-862-7451

Query Match 1.7%; Score 59; DB 9; Length 326;
Best Local Similarity 58.1%; Pred. No. 1.8e-06;
Matches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGACGATCTTCCGAGACGCTGTTCTTCAAGTTCT 2669
DB 180 TGGAGTGAATTTTAAAAATGGATGATTTACGACAGATATGTTGACACTCAATGTT 121

QY 2670 CGAAGTATGATTAATCTGGAGAGCTGCAAAATGATTCCTGTTGAAACCGTACGC 2729
 DB 120 GGGCTTATGATTAATCTGGAGAGCTGTTGATTCCTGGATTCCTTATG 61
 QY 2730 ACTTTTCAATGGAGAAATGATTTGAAATTTGAGTTGCTTAATTTGAAACAA 2788
 DB 60 CTGTTTACCAACAGAGATTCCTGCTGAGCTTCAATGAGTGTGAGACCTTGAAACAA 2

RESULT 11

US-09-921-232-1
 ; Sequence 1, Application US/09921232
 ; Patent No. US20020102681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; FILE REFERENCE: 0706D4
 ; CURRENT APPLICATION NUMBER: US/09/921,232
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (258)...(2666)
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(3252)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-921-232-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 2976 TGAAGTGTGATGATTCCTTACTCGTGTGTTGATTTGATTTGCACTGACATATAT 3035
 DB 2168 TCAATGTTTGAGACATTTCAAAAAGCTGCGGCTTACTCTGTCATTACATATAT 2227
 QY 3036 GGGATCAAGATCTGCAAGATATCTGATGCTCACTGAAGATGAAATATATGTC 3095
 DB 2228 GGGGGTGGAGACAGGATCTGATATCTTTCTTAAGTATGATGACGCTTTTCA 2287
 QY 3096 CATGATTTGGTCACTTTTGGGAC 3121
 DB 2288 TGTGACTTTGCTTTATCTCTGGGC 2313

RESULT 12

US-09-921-330-1
 ; Sequence 1, Application US/09921330
 ; Patent No. US20020102682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; FILE REFERENCE: 0706D4
 ; CURRENT APPLICATION NUMBER: US/09/921,330
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays

FILE REFERENCE: 0706D3
 ; CURRENT APPLICATION NUMBER: US/09/921,330
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (258)...(2666)
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(3252)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-921-330-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 2976 TGAAGTGTGATGATTCCTTACTCGTGTGTTGATTTGATTTGCACTGACATATAT 3035
 DB 2168 TCAATGTTTGAGACATTTCAAAAAGCTGCGGCTTACTCTGTCATTACATATAT 2227
 QY 3036 GGGATCAAGATCTGCAAGATATCTGATGCTCACTGAAGATGAAATATATGTC 3095
 DB 2228 GGGGGTGGAGACAGGATCTGATATCTTTCTTAAGTATGATGACGCTTTTCA 2287
 QY 3096 CATGATTTGGTCACTTTTGGGAC 3121
 DB 2288 TGTGACTTTGCTTTATCTCTGGGC 2313

RESULT 13

US-09-921-329-1
 ; Sequence 1, Application US/09921329
 ; Patent No. US20020110884A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; FILE REFERENCE: 0706D2
 ; CURRENT APPLICATION NUMBER: US/09/921,329
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays

FEATURE:
 NAME/KEY: CDS
 LOCATION: (258)...(2666)
 NAME/KEY: misc_feature
 LOCATION: (1)...(3252)
 OTHER INFORMATION: n = A,T,C or G
 US-09-921-329-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 2976 TGAAGTGCATGCTGCTTACCGTGTGGATGATTCAGTTGCCACGACATAT 3035
 DB 2168 TCAATGTTGAGACATTTATAAAGCTGCCCGGTTACTCTGTCATTACATAT 2227
 QY 3036 GGAATCAAGATCGTCACAGTATATCTGATGCTCACTGAAGTGAATAATGTCCA 3095
 DB 2228 GGGGGTTGAGACAGGACATCTGATATCTTCTTCACTGATGAGCGCTTTTCA 2287
 QY 3096 CATTGATTCGGTCACATTTGGGAC 3121
 DB 2288 TGTGACTTTCCTTATCTCTGGGC 2313

RESULT 14

US-09-771-161A-10
 Sequence 10, Application US/09771161A
 Patent No. US2002011081A1
 GENERAL INFORMATION:

APPLICANT: LEVINE, et al.
 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 FILE REFERENCE: 802620-2005.1
 CURRENT APPLICATION NUMBER: US/09/771,161A
 PRIOR FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 09/724,676
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 136776
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 135619
 PRIOR FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 273
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 10
 LENGTH: 2418
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-771-161A-10

Query Match 1.2%; Score 42.8; DB 10; Length 2418;
 Best Local Similarity 53.6%; Pred. No. 0.32; 77; Indels 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 2608 TGTGCAATGATCTTCAAGATGAGAGATCTTCCGACAGATGCTGTTCTTCAAGTT 2667
 DB 1938 TATCCAGTATATTTAAGATGAGATGATTTTACGTCAGATCACTTATCTTCAATC 1997
 QY 2668 CTCGAAGTATGATTAACATCTGGAAGCTGCAACATGATGCTGTTGAACCCGTAC 2727
 DB 1998 ATTTCACATGACACAGCTGTACCGAAGAAATCTGACTTGAATGACACCTTAT 2057
 QY 2728 GCAGTCTTCCATGGGAGAAATGATGGAATTAATGAGTTCTGC 2773
 DB 2058 AAGGTGTAGCCACAGTACAAACATGCTTATGACAGTTATTC 2103

RESULT 15

US-09-801-368-389
 Sequence 389, Application US/09801368
 Patent No. US20020128250A1
 GENERAL INFORMATION:
 APPLICANT: Busby, Robert
 APPLICANT: Cali, Brian

APPLICANT: Hecht, Peter
 APPLICANT: Holtzman, Doug
 APPLICANT: Madden, Kevin
 APPLICANT: Maxon, Mary
 APPLICANT: Milne, Todd
 APPLICANT: No. US20020128250A1man, Thea
 APPLICANT: Royer, John
 APPLICANT: Salama, Sofie
 APPLICANT: Sherman, Amir
 APPLICANT: Silva, Jeff
 APPLICANT: Summers, Eric
 TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 FILE REFERENCE: 109272.147
 CURRENT APPLICATION NUMBER: US/09/801,368
 PRIOR APPLICATION NUMBER: US 09/487,558
 PRIOR FILING DATE: 2000-01-19
 PRIOR APPLICATION NUMBER: US 60/160,587
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 440
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 389
 LENGTH: 5703
 TYPE: DNA
 ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-389

Query Match 1.2%; Score 42.2; DB 10; Length 5703;
 Best Local Similarity 58.3%; Pred. No. 0.84;
 Matches 74; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 2992 TTCCTATCTGCTGTGATGATTCAGTTGCCAGTCAATPAATGGATCAAGATGCT 3051
 DB 5206 TTGTTAATCTTATGCGGATATAGCGTAATTTGATTTGTTGCAATTCAGGATAGA 5265
 QY 3052 CACAGTGAATATCTGATGCTCACTGAAGATGGAATAATGTCCACATTTGCTGTCAC 3111
 DB 5266 CATATGTAATATATGATGATGATCAAGACATTTCTACATATGATTTTGGGTTT 5325
 QY 3112 ATTTTGG 3118
 DB 5326 ATTTTGG 5332

Search completed: June 6, 2003, 05:11:19
 Job time: 503 secs